

Score over length search

ACCESS DB #

184133

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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 4/4/06
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 101643,038
Location (Bldg/Room#): 2d28 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

Ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: AS MODR of h. PLA₂, group A

Inventors (please provide full names): Bennett et al

Earliest Priority Date: 5-25-01

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 17

between bases 994 - 1070 only

between

• Size limit to 8-50 Nucleobases

• Score over length search

• No Interference please

~~Therese~~

• 70% Identity or greater

17-1080 na

Therese

EST-8
ge-182
iss-100
nqa 299
pubmain 119
pubnew 351

1d2
BOB

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SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70% , *length 8-50 nt*

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 16:13:31 ; Search time 0.001 Seconds
(without alignments)
334.488 Million cell updates/sec

Title: US-10-643-038-17_994-1070

Perfect score: 77

Sequence: 1 caaacaagacgcctgggga.....gaagctgctgtctgaag 77

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 119 seqs, 2172 residues

Total number of hits satisfying chosen parameters: 238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 119 summaries

Database : pubmaindb.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	25	32.5	25	1	US-10-956-157-18260, A
2	25	32.5	25	1	US-10-956-157-157048
3	25	32.5	25	1	US-10-956-157-169708
4	25	32.5	25	1	US-11-060-756-94739
5	25	32.5	25	1	US-11-060-756-94763
6	24	31.2	25	1	US-10-956-157-150028
7	22	28.6	25	1	US-10-956-157-170149
8	21	27.3	25	1	US-10-956-157-141304
9	21	27.3	25	1	US-10-956-157-160508
10	21	27.3	25	1	US-11-060-756-152285
11	20	26.0	20	1	US-09-865-866-19
12	20	26.0	20	1	US-09-865-866-20
13	20	26.0	20	1	US-09-865-866-21
14	20	26.0	20	1	US-09-865-866-22
15	20	26.0	20	1	US-09-865-866-23
16	20	26.0	20	1	US-09-865-866-24
17	20	26.0	20	1	US-09-865-866-25
18	20	26.0	20	1	US-10-643-038-19
19	20	26.0	20	1	US-10-643-038-20
20	20	26.0	20	1	US-10-643-038-21
21	20	26.0	20	1	US-10-643-038-22
22	20	26.0	20	1	US-10-643-038-23
23	20	26.0	20	1	US-10-643-038-24
24	20	26.0	20	1	US-10-643-038-25
25	17.8	23.1	21	1	US-10-847-918-6072
26	17.8	23.1	25	1	US-11-036-317-81949
27	17.8	23.1	25	1	US-11-036-317-589182
28	17.6	22.9	25	1	US-10-719-956-632892
29	17.6	22.9	25	1	US-10-719-900-154278
30	17.6	22.9	25	1	US-10-719-900-338409
31	17	22.1	20	1	US-10-422-475-4
32	16.8	21.8	21	1	US-10-847-918-5566
33	16.8	21.8	21	1	US-10-847-918-5568

34	16.8	21.8	21	1	US-10-847-918-6070	Sequence 6070, Ap
35	16.4	21.3	21	1	US-10-847-918-5567	Sequence 5567, Ap
36	16.4	21.3	21	1	US-10-847-918-5569	Sequence 5569, Ap
C 37	16.4	21.3	21	1	US-10-847-918-5571	Sequence 5571, Ap
38	16.4	21.3	21	1	US-10-847-918-6071	Sequence 6071, Ap
39	15.4	20.0	21	1	US-10-847-918-5570	Sequence 5570, Ap
40	15.4	20.0	22	1	US-10-509-738-15	Sequence 15, Appl
C 41	15.2	19.7	21	1	US-10-751-736-9539	Sequence 9539, Ap
C 42	14.8	19.2	21	1	US-10-751-736-16743	Sequence 16743, A
C 43	14.8	19.2	21	1	US-10-751-736-17280	Sequence 17280, A
C 44	14.8	19.2	21	1	US-10-679-366-14	Sequence 14, Appl
45	14.8	19.2	21	1	US-10-847-918-5564	Sequence 5564, Ap
46	14.4	18.7	17	1	US-09-866-108-10026	Sequence 10026, A
47	14.4	18.7	17	1	US-09-866-108-10027	Sequence 10027, A
48	14.4	18.7	17	1	US-10-723-361-10026	Sequence 10026, A
49	14.4	18.7	17	1	US-10-723-361-10027	Sequence 10027, A
50	14	18.2	17	1	US-09-866-108-10024	Sequence 10024, A
51	14	18.2	17	1	US-09-866-108-10025	Sequence 10025, A
52	14	18.2	17	1	US-10-723-361-10024	Sequence 10024, A
53	14	18.2	17	1	US-10-723-361-10025	Sequence 10025, A
C 54	13.8	17.9	17	1	US-09-866-108-930	Sequence 930, App
55	13.4	17.4	17	1	US-09-866-108-10028	Sequence 10028, A
C 56	13.4	17.4	17	1	US-10-060-998-931	Sequence 931, App
C 57	13.4	17.4	17	1	US-10-060-998-932	Sequence 932, App
58	13.4	17.4	17	1	US-10-723-361-10028	Sequence 10028, A
C 59	13.2	17.1	18	1	US-09-776-191-56	Sequence 56, Appl
C 60	13.2	17.1	18	1	US-10-092-004A-6	Sequence 6, Appl
61	13	16.9	17	1	US-09-866-108-10023	Sequence 10023, A
62	13	16.9	17	1	US-10-723-361-10023	Sequence 10023, A
C 63	13	16.9	18	1	US-10-367-980A-11	Sequence 11, Appl
C 64	12.8	16.6	17	1	US-10-060-998-929	Sequence 929, App
65	12.8	16.6	18	1	US-10-469-277-7	Sequence 7, Appl
66	12.4	16.1	17	1	US-09-866-108-10029	Sequence 10029, A
67	12.4	16.1	17	1	US-09-825-805-816	Sequence 816, App
C 68	12.4	16.1	17	1	US-10-060-998-927	Sequence 927, App
C 69	12.4	16.1	17	1	US-10-060-998-928	Sequence 928, App
C 70	12.4	16.1	17	1	US-10-060-998-933	Sequence 933, App
71	12.4	16.1	17	1	US-10-163-552-786	Sequence 786, App
72	12.4	16.1	17	1	US-10-138-674-7914	Sequence 7914, Ap
73	12.4	16.1	17	1	US-10-287-949A-7914	Sequence 7914, A
74	12.4	16.1	17	1	US-10-723-361-10029	Sequence 10029, A
75	12.4	16.1	17	1	US-10-712-633-1056	Sequence 1056, Ap
76	12.4	16.1	17	1	US-10-724-270-5441	Sequence 5441, Ap
C 77	12.2	15.8	17	1	US-09-864-785-2825	Sequence 2825, Ap
C 78	12.2	15.8	17	1	US-09-930-423-1056	Sequence 1056, Ap
79	12.2	15.8	17	1	US-09-745-237A-1056	Sequence 1056, Ap
C 80	12.2	15.8	17	1	US-10-138-674-8872	Sequence 8872, Ap
C 81	12.2	15.8	17	1	US-10-287-949A-8872	Sequence 8872, Ap
C 82	12.2	15.8	17	1	US-10-712-633-4058	Sequence 4058, Ap
83	12.2	15.8	17	1	US-10-913-280-108	Sequence 108, App
84	12	15.6	16	1	US-10-776-934-113	Sequence 113, App
85	12	15.6	16	1	US-10-776-934-592	Sequence 592, App
86	12	15.6	16	1	US-10-776-934-593	Sequence 593, App
87	12	15.6	16	1	US-10-776-934-594	Sequence 594, App
88	12	15.6	16	1	US-10-776-934-595	Sequence 595, App
89	12	15.6	17	1	US-09-866-108-10022	Sequence 10022, A
90	12	15.6	17	1	US-10-723-361-10022	Sequence 10022, A
C 91	11.8	15.3	16	1	US-10-138-674-6986	Sequence 6986, Ap
C 92	11.8	15.3	16	1	US-10-287-949A-6986	Sequence 6986, Ap
C 93	11.8	15.3	16	1	US-10-741-600-73537	Sequence 73537, A
C 94	11.4	14.8	13	1	US-10-257-0178-41787	Sequence 41787, A
C 95	11.4	14.8	13	1	US-10-257-0178-18441	Sequence 18441, A
C 96	11.4	14.8	13	1	US-10-257-0178-18441	Sequence 18441, A
C 97	11.4	14.8	13	1	US-10-257-0178-18442	Sequence 18442, A
C 98	11.4	14.8	16	1	US-10-142-729-26	Sequence 26, Appl
C 99	11.4	14.8	16	1	US-10-142-729-39	Sequence 39, Appl
C 100	11.4	14.8	16	1	US-10-375-504-26	Sequence 26, Appl
C 101	11.4	14.8	16	1	US-10-375-504-39	Sequence 39, Appl
C 102	11.4	14.8	16	1	US-10-719-993-55182	Sequence 55182, A
C 103	11.2	14.5	16	1	US-09-875-453-65	Sequence 65, Appl
C 104	11.2	14.5	16	1	US-10-331-907-450	Sequence 450, Appl
C 105	11.2	14.5	16	1	US-10-407-807-67	Sequence 67, Appl
C 106	11	14.3	11	1	US-10-450-797-548	Sequence 548, App

c 107 11 14.3 12 1 US-10-257-017B-320928 Sequence 320928,
c 108 11 14.3 13 1 US-10-257-017B-14593 Sequence 14593, A
c 109 11 14.3 13 1 US-10-257-017B-14594 Sequence 14594, A
c 110 11 14.3 13 1 US-10-257-017B-181997 Sequence 181997,
c 111 11 14.3 13 1 US-10-257-017B-181998 Sequence 181998,
c 112 11 14.3 13 1 US-10-257-017B-224917 Sequence 224917,
c 113 11 14.3 13 1 US-10-257-017B-224918 Sequence 224918,
c 114 11 14.3 14 1 US-09-998-027-20 Sequence 20, Appl
c 115 11 14.3 14 1 US-10-165-099-20 Sequence 20, Appl
c 116 11 14.3 15 1 US-09-504-231A-1178 Sequence 1178, Ap
c 117 11 14.3 15 1 US-09-504-231A-1179 Sequence 1179, Ap
c 118 11 14.3 15 1 US-09-274-553D-1178 Sequence 1178, Ap
c 119 11 14.3 15 1 US-09-274-553D-1179 Sequence 1179, Ap

ALIGNMENTS

RESULT 1
US-10-956-157-18260
; Sequence 18260, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18260
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-18260

Query Match 32.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GATACAACTCTGGAGTCTCTGAGA 43
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DB 1 GATACAACTCTGGAGTCTCTGAGA 25

RESULT 2
US-10-956-157-157048
; Sequence 157048, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 157048
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-157048

Query Match 32.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AACACAGCGCCTGGGATCAACT 27
|||||

Db 1 AACACAGCGCCTGGGATCAACT 25
RESULT 3
US-10-956-157-169708
; Sequence 169708, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 169708
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-169708

Query Match 32.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAAGACGGCCTGGGATCAACTCT 29
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DB 1 CAAGACGGCCTGGGATCAACTCT 25

RESULT 4
US-11-060-756-94739
; Sequence 94739, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94739
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-94739

Query Match 32.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GATACAACTCTGGAGTCTCTGAGA 43
|||||
DB 1 GATACAACTCTGGAGTCTCTGAGA 25

RESULT 5
US-11-060-756-94763
; Sequence 94763, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18

; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94763
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe
US-11-060-756-94763

Query Match 32.5%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTCTCTGAG 42
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Db 1 GGATACAACTCTGGAGTCTCTGAG 25

RESULT 6

US-10-956-157-150028
; Sequence 150028, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 150028
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-150028

Query Match 31.2%; Score 24; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAACAGACGGCTGGGATACA 24
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Db 2 CAAACAGACGGCTGGGATACA 25

RESULT 7

US-10-956-157-170149
; Sequence 170149, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170149
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-170149

Query Match 28.6%; Score 22; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CAACTCTGGAGTCTCTGAGAG 44
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CAACTCTGGAGTCTCTGAGAG 22

RESULT 8

US-10-956-157-141304
; Sequence 141304, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141304
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-141304

Query Match 27.3%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAACAGACGGCTGGGAT 21
| | | | | | | | | | | | | | | | | | | | | |
Db 5 CAAACAGACGGCTGGGAT 25

RESULT 9

US-10-956-157-160508
; Sequence 160508, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160508
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-160508

Query Match 27.3%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 AACTCTGGAGTCTCTGAGAG 44
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AACTCTGGAGTCTCTGAGAG 21

RESULT 10

US-11-060-756-152285
; Sequence 152285, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152285
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-152285
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Query Match      27.3%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 24 AACTCTGGAGTCTCTCGAG 44
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Db 1 AACTCTGGAGTCTCTCGAG 21
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RESULT 11
US-09-865-866-19/c
; Sequence 19, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-19
```

```
Query Match      26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CAACACAGACGGCTGGGA 20
      |||||
Db 20 CAACACAGACGGCTGGGA 1
```

```
RESULT 12
US-09-865-866-20/c
; Sequence 20, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-20
```

```
Query Match      26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 12 GCCTGGGATACAACTCTGG 31
      |||||
Db 20 GCCTGGGATACAACTCTGG 1
```

```
RESULT 13
US-09-865-866-21/c
; Sequence 21, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-21
```

```
Query Match      26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 23 CAACTCTGGAGTCTCTGAG 42
      |||||
Db 20 CAACTCTGGAGTCTCTGAG 1
```

```
RESULT 14
US-09-865-866-22/c
; Sequence 22, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-22
```

```
Query Match      26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 33 GTCCTCTGAGAGGTAAGAG 52
      |||||
Db 20 GTCCTCTGAGAGGTAAGAG 1
```

```
RESULT 15
US-09-865-866-23/c
; Sequence 23, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 23
; LENGTH: 20
```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-23

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 CTCGAGAGGTAAAGAGCCA 55
Db 20 CTCGAGAGGTAAAGAGCCA 1

RESULT 16
US-09-866-24/c
; Sequence 24, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-24

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AGAGGTTAAAGCCAGCGCAA 60
Db 20 AGAGGTTAAAGCCAGCGCAA 1

RESULT 17
US-09-866-25/c
; Sequence 25, Application US/09865866
; Publication No. US20030045487A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/09/865,866
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-865-866-25

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTGTCAAG 77
Db 20 GAAGCTGATGTCCTGTCAAG 1

RESULT 18
US-10-643-038-19/c
; Sequence 19, Application US/10643038
; Publication No. US2005014331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-19

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAACAGACGGCTGGGA 20
Db 20 CAAACAGACGGCTGGGA 1

RESULT 19
US-10-643-038-20/c
; Sequence 20, Application US/10643038
; Publication No. US2005014331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-20

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GCCTGGGGATACAACTCTGG 31
Db 20 GCCTGGGGATACAACTCTGG 1

RESULT 20
US-10-643-038-21/c
; Sequence 21, Application US/10643038
; Publication No. US2005014331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RFS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; CURRENT FILING DATE: 2003-08-18

; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-21

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CAACCTCTGGAGTCTCTGAG 42
Db 20 CAACCTCTGGAGTCTCTGAG 1

RESULT 21
US-10-643-038-22/c
; Sequence 22, Application US/10643038
; Publication No. US20050143331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-22

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTCTCTGAGAGGTAAGAG 52
Db 20 GTCTCTGAGAGGTAAGAG 1

RESULT 22
US-10-643-038-23/c
; Sequence 23, Application US/10643038
; Publication No. US20050143331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-23

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CTCTGAGAGGTAAGAGCCA 55
Db 20 CTCTGAGAGGTAAGAGCCA 1

RESULT 23
US-10-643-038-24/c
; Sequence 24, Application US/10643038
; Publication No. US20050143331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-24

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTAAGAGCCAGCAA 60
Db 20 AGAGGTAAGAGCCAGCAA 1

RESULT 24
US-10-643-038-25/c
; Sequence 25, Application US/10643038
; Publication No. US20050143331A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
; FILE REFERENCE: RTS-0221
; CURRENT APPLICATION NUMBER: US/10/643,038
; PRIOR FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/865,866
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-038-25

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCTGTCAAG 77
Db 20 GAAGCTGATGTCTGTCAAG 1

RESULT 25
US-10-847-918-6072/c

```
; Sequence 6072, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AMI01264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6072
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-antisense strand
; US-10-847-918-6072

Query Match      23.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 AAGAGCCAGCGAGCTGATGT 68
Db 21 AAAAGCCAGCGAGCTGATGT 1

RESULT 26
US-11-036-317-81949/c
; Sequence 81949, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-81949

Query Match      23.1%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 51 AGCCAGCGAGCTGATGCTCT 71
Db 23 AGCCAGCGAGCTGATGCTACT 3

RESULT 27
US-11-036-317-589182/c
; Sequence 589182, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
```

```
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 589182
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-589182

Query Match      23.1%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 24;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 20 ATACAACCTCTGGAGTCTCTG 40
Db 22 ATACAACGCTGGAGTCTCTATG 2

RESULT 28
US-10-719-956-632892/c
; Sequence 632892, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 632892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-632892

Query Match      22.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAGCTGATGTC 70
Db 25 AAAGAGCGAGCGAAGTTGTTGGCC 2

RESULT 29
US-10-719-900-154278/c
; Sequence 154278, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 154278
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-154278

Query Match      22.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 46 TAAAGAGCGAGCGAAGCTGATGTC 69
```

```
Db      25  TAAAGAGCGCAGCGAGCTCAGCTC 2
RESULT 30
US-10-719-900-338409
; Sequence 338409, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 338409
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-338409
Query Match      22.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      26  CTCTGGAGTCTCTGAGAGGTAAA 49
          ||||| ||||| ||||| |||||
Db      2  CACTGGAGGCTCTGACAGGGNAA 25

RESULT 31
US-10-422-475-4
; Sequence 4, Application US/10422475
; Publication No. US20030235813A1
; GENERAL INFORMATION:
; APPLICANT: Luyten, Frank
; APPLICANT: De Bari, Cosimo
; APPLICANT: Dell'Accio, Francesco
; TITLE OF INVENTION: In vivo assay and molecular markers for testing the phenotypic
; TITLE OF INVENTION: stability of cell populations and selecting cell populations for
; TITLE OF INVENTION: autologous transplantation
; FILE REFERENCE: T2420-US
; CURRENT APPLICATION NUMBER: US/10/422,475
; CURRENT FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/375,218
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: EP 99203273.0
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: RASP-A PLA2      sense primer
US-10-422-475-4
Query Match      22.1%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23  CAACTCTGGAGTCTCTCT 39
          ||||| ||||| ||||| |||||
Db      4  CAACTCTGGAGTCTCTCT 20

RESULT 32
US-10-847-918-5566
; Sequence 5566, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5566
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-5566
Query Match      21.8%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      49  AGAGCCAGCGAGCTGATGT 68
          ||||| ||||| ||||| |||||
Db      1  AAAGCCAGCGACGCTGATGT 20

RESULT 33
US-10-847-918-5568/c
; Sequence 5568, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5568
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-antisense strand
US-10-847-918-5568
Query Match      21.8%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      49  AGAGCCAGCGAGCTGATGT 68
          ||||| ||||| ||||| |||||
Db      21  AAAGCCAGCGACGCTGATGT 2

RESULT 34
US-10-847-918-6070
; Sequence 6070, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
```



```
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6070
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-6070

Query Match      21.8%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 49 AGAGCCAGCGAGCTGATGT 68
| | | | | | | | | | | | | | | | | | | | |
Db 2 AAAGCCAGCGAGCTGATGT 21

RESULT 35
US-10-847-918-5567
; Sequence 5567, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5567
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-sense strand
US-10-847-918-5567

Query Match      21.3%; Score 16.4; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAGCTGATGT 68
| | | | | | | | | | | | | | | | | | | | |
Db 1 AGCCAGCGAGCTGATGT 18

RESULT 36
US-10-847-918-5569
; Sequence 5569, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
```

```
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5569
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-5569

Query Match      21.3%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAGCTGATGT 68
| | | | | | | | | | | | | | | | | | | | |
Db 2 AGCCAGCGAGCTGATGT 19

RESULT 37
US-10-847-918-5571/c
; Sequence 5571, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5571
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-antisense strand
US-10-847-918-5571

Query Match      21.1%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAGCTGATGT 68
| | | | | | | | | | | | | | | | | | | | |
Db 20 AGCCAGCGAGCTGATGT 3

RESULT 38
US-10-847-918-6071
; Sequence 6071, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6071
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-sense strand
US-10-847-918-6071
```

```
Query Match      21.3%; Score 16.4; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 51 AGCCAGCGAAGCTGATGT 68
||||||| |||||
Db 2 AGCCAGCGACGUGAUGU 19

RESULT 39
US-10-847-918-5570
; Sequence 5570, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5570
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai-sense strand
US-10-847-918-5570

Query Match      20.0%; Score 15.4; DB 1; Length 21;
Best Local Similarity 76.5%; Pred. No. 34;
Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 52 GCCAGCGAAGCTGATGT 68
||||||| |||||
Db 1 GCCAGCGACGUGAUGU 17

RESULT 40
US-10-509-738-15
; Sequence 15, Application US/10509738
; Publication No. US2005020431A1
; GENERAL INFORMATION:
; APPLICANT: Director-General of National Institute of Advanced Industrial Science and Technology; Info Genes Co., Ltd.; Kazusa DNA Research Institute
; TITLE OF INVENTION: Application of KIAA0172 gene functions for therapeutics, diagnostics and pharmaceuticals
; FILE REFERENCE: PH-1610-PCT
; CURRENT APPLICATION NUMBER: US/10/509,738
; CURRENT FILING DATE: 2004-09-30
; PRIOR APPLICATION NUMBER: JP 2002/99422
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-509-738-15

Query Match      20.0%; Score 15.4; DB 1; Length 22;
Best Local Similarity 94.1%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 60 AGCTGATGCTCTGTCAA 76
||||||| |||||||
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```
Db 2 AGCTGATGCTCTGTCAA 18

RESULT 41
US-10-751-736-9539/c
; Sequence 9539, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
US-10-751-736-9539

Query Match      19.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 24 AACTCTGGAGTCTCTGAGA 43
||||||| |||||||
Db 21 AACTCAGGAGTCTCTGAGAGA 2

RESULT 42
US-10-751-736-16743/c
; Sequence 16743, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON CANCERS
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16743
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
US-10-751-736-16743

Query Match      19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 31 GACTCCTCTGAGAGGTAA 48
||||||| |||||||
Db 18 GATTACTCTGAGAGGTAA 1

RESULT 43
US-10-751-736-17280/c
; Sequence 17280, Application US/10751736
; Publication No. US20040265230A1
```

; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751.736
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17280
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-17280

Query Match 19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 31 GAGTCCTCTGAGAGTTAA 48
Db 18 GATTACTCTGAGAGTTAA 1

RESULT 44
US-10-679-366-14/c
; Sequence 14, Application US/10679366
; Publication No. US20050059025A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Wei
; APPLICANT: Wu, Leeyang
; TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL HUMAN
; FILE REFERENCE: AM101072
; CURRENT APPLICATION NUMBER: US/10/679,366
; CURRENT FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-679-366-14

Query Match 19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 24 AACTCTGAGTCCTCTCA 41
Db 21 AAGTCAGAGTCCTCTCA 4

RESULT 45
US-10-847-918-5564
; Sequence 5564, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729

; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5564
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-5564

Query Match 19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 49 AGAGCCAGCGAGCTGAT 66
Db 3 AAGCCAGCGAGCGAGT 20

RESULT 46
US-09-866-108-10026
; Sequence 10026, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 10026
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10026

Query Match 18.7%; Score 14.4; DB 1; Length 17;

; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-866-108-10025

Query Match 18.2%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCG 40
 Db 3 TCTGGAGTCTCTCG 16

RESULT 52

US-10-723-361-10024
 ; Sequence 10024, Application US/10723361
 ; Publication No. US20040137589A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
 ; APPLICANT: JI, Yonggang
 ; APPLICANT: PENN, Sharron G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723,361

; PRIOR FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 10024

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-361-10024

Query Match

Best Local Similarity 18.2%; Score 14; DB 1; Length 17;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCG 40
 Db 4 TCTGGAGTCTCTCG 17

RESULT 53

US-10-723-361-10025

; Sequence 10025, Application US/10723361

; Publication No. US20040137589A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; APPLICANT: JI, Yonggang
 ; APPLICANT: PENN, Sharron G.
 ; APPLICANT: HANZEL, David K.
 ; APPLICANT: RANK, David R.
 ; APPLICANT: CHEN, Wensheng
 ; APPLICANT: SHANNON, Mark
 ; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723,361

; PRIOR FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 10025

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-361-10025

Query Match

Best Local Similarity 18.2%; Score 14; DB 1; Length 17;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCG 40
 Db 3 TCTGGAGTCTCTCG 16

RESULT 54

US-10-060-998-930/c

; Sequence 930, Application US/10060998

; Publication No. US20030104530A1

; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong

; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1

; FILE REFERENCE: PB01108

; CURRENT APPLICATION NUMBER: US/10/060,998

; PRIOR FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 09/864,761

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/343,331

; PRIOR FILING DATE: 2001-12-21

; NUMBER OF SEQ ID NOS: 3056

; SOFTWARE: Aecomica Sequence Listing Engine

; SEQ ID NO 930

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-060-998-930

Query Match

17.9%; Score 13.8; DB 1; Length 17;

```
Best Local Similarity 88.2%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAGCT 63
Db 17 AATGAGCCAGCGAAGAT 1

RESULT 55
US-09-866-108-10028
; Sequence 10028, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; FILE REFERENCE: PBO1108
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wenaheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866.108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10028
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10028

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGAGTCTCTGTGAG 42
Db 1 CTGAGTCTCTGTG 15

RESULT 56
US-10-060-998-931/c

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
; Sequence 931, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; FILE REFERENCE: PBO1108
; APPLICANT: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 931
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-931

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAAG 61
Db 16 AATGAGCCAGCGAAG 2

RESULT 57
US-10-060-998-932/c

; Sequence 932, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PBO1108
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 932
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-932

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 40;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAAG 61
Db 15 AATGAGCCAGCGAAG 1

RESULT 58
US-10-723-361-10028
; Sequence 10028, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
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; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10023
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10023

Query Match      16.9%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 TCTGGAGTCTCTCT 39
DB      5 TCTGGAGTCTCTCT 17

RESULT 62
US-10-723-361-10023
; Sequence 10023, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN
; CURRENT APPLICATION NUMBER: US/10/723,361
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 10023
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10023

Query Match      16.9%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 TCTGGAGTCTCTCT 39
DB      5 TCTGGAGTCTCTCT 17

RESULT 63
US-10-367-980A-11/c
; Sequence 11, Application US/10367980A
; Publication No. US20030228592A1
; GENERAL INFORMATION:
; APPLICANT: St Vincent's Institute of Medical Research
; APPLICANT: Rogers, Suzanne D
; APPLICANT: Best, James D
; TITLE OF INVENTION: Human Facilitative Glucose Transport Protein GLUT8
; FILE REFERENCE: VS:AJH:FP17928
; CURRENT APPLICATION NUMBER: US/10/367,980A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 09/509,731
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: PCR primer (reverse)
US-10-367-980A-11

Query Match      16.9%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      50 GAGCCAGCGAAGC 62
DB      14 GAGCCAGCGAAGC 2

RESULT 64
US-10-060-998-929/c
; Sequence 929, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 929
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-929

Query Match      16.6%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;

QY 48 AAGAGCCAGCGAAGCT 63
Db 17 ATGAGCCAGCGAAGAT 2

RESULT 65
US-10-469-277-7
; Sequence 7, Application US/10469277
; Publication No. US20040170996A1
; GENERAL INFORMATION:
; APPLICANT: Yee, Leland
; APPLICANT: Tang, Jianming
; APPLICANT: Kaslow, Richard A.
; APPLICANT: van Leeuwen, Dirk J.
; TITLE OF INVENTION: CYTOTOXIC T-LYMPHOCYTE ANTIGEN-4 OR INTERLEUKIN-10 POLYMORPHISMS
; TITLE OF INVENTION: AS PREDICTORS OF RESPONSE TO THERAPEUTIC INTERVENTION
; FILE REFERENCE: UAB-19302/22
; CURRENT APPLICATION NUMBER: US/10/469,277
; CURRENT FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: PCT/US02/06207
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/271,811
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Reverse primer
US-10-469-277-7

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 52;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;

QY 47 AAGAGCCAGCGAAGC 62
Db 1 ACAGAGCCAGCGCAAGC 16

RESULT 66
US-09-866-108-10029
; Sequence 10029, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108

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; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10029
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10029

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTGAG 42
Db 1 TGGAGTCCTCTGTG 14

RESULT 67
US-09-825-805-816
; Sequence 816, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MEH800-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675

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; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 816
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-816

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGAGTCTCTGA 41
Db 4 CUGAGCCCUUGA 17

RESULT 68
US-10-060-998-927/c
; Sequence 927, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 927
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-927

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCT 63
Db 17 GAGCCAGCGAAGAT 4

RESULT 69
US-10-060-998-928/c
; Sequence 928, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 927
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-927
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; SEQ ID NO 928
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-928

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCT 63
Db 16 GAGCCAGCGAAGAT 3

RESULT 70
US-10-060-998-933/c
; Sequence 933, Application US/10060998
; Publication No. US20030104530A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: HUMAN SODIUM-HYDROGEN EXCHANGER LIKE PROTEIN 1
; FILE REFERENCE: PB01108
; CURRENT APPLICATION NUMBER: US/10/060,998
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/343,331
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 3056
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 933
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-998-933

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAA 60
Db 14 AATGAGCCAGCGAA 1

RESULT 71
US-10-163-552-786
; Sequence 786, Application US/10163552
; Publication No. US20030105051A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
; TITLE OF INVENTION: HER2
; FILE REFERENCE: MBH01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 786
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-163-552-786

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGAGTCTCTGA 41
```

Db 4 CUGGAGCCUCUGA 17
|:||||| |:|:|

RESULT 72

US-10-138-674-7914
; Sequence 7914, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7914
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7914

Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 52;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCCTCT 39
|:||||| |:|:|

Db 2 CUCGGAGGAGUCCUCU 15

RESULT 73

US-10-287-949A-7914
; Sequence 7914, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7914
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7914

Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 52;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCCTCT 39
|:||||| |:|:|

Db 2 CUCGGAGGAGUCCUCU 15

RESULT 74

US-10-723-361-10029
; Sequence 10029, Application US/10723361
; Publication No. US20040137589A1
; GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART ANI
; FILE REFERENCE: PB0105
; CURRENT APPLICATION NUMBER: US/10/723,361
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 09/866,108
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; SEQ ID NO 10029
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-361-10029

Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCCTCTGAG 42

Db 1 TGGAGTCCTCTGAG 14

RESULT 75

US-10-712-633-1056
; Sequence 1056, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTO
; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND C
; FILE REFERENCE: MBHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07

; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1056
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-1056

Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 64.3%; Pred. No. 52;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCCTGGAGTCCTCT 39
|:|:|:|:|:|:|:|:
Db 2 CUCGGAGGUCCUCU 15

RESULT 76

US-10-724-270-5441
; Sequence 5441, Application US/10724270
; Publication No. US2005080031A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level
; TITLE OF INVENTION: RAS, HER2 and HIV
; FILE REFERENCE: 400/046-US (MEHB02-326-A)
; CURRENT APPLICATION NUMBER: US/10/724,270
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: PCT/US02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/294,140
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 10/238,700
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 10/157,580
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 10/693,059
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 10/444,853
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 10/417,012
; PRIOR FILING DATE: 2003-04-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 6810
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5441
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-724-270-5441

Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 52;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTCGAGTCCTCTGA 41
|:|:|:|:|:|:|:|:
Db 4 CUGGAGCCUCUGA 17

RESULT 77
US-09-864-785-2825/c
; Sequence 2825, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Draper, Ken
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of NF-Kappa B
; FILE REFERENCE: 400/022 (MEHB00-812-D)
; CURRENT APPLICATION NUMBER: US/09/864,785
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 3929
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2825
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-864-785-2825

Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 55;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AAGACGCCCTGGGATA 22
|:|:|:|:|:|:|:|:
Db 17 AGGAGGCCCTGGGCTA 1

RESULT 78

US-09-930-423-1056
; Sequence 1056, Application US/09930423
; Publication No. US2003002003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MEHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1056
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1056

Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 55;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 61 GCTGATGTCCTGTCAG 77
|:|:|:|:|:|:|:|:
Db 1 GCUGGUGGUCGCGCAAG 17

RESULT 79

US-09-745-237A-1056
; Sequence 1056, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MEHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A

```

; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1056
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1056

```

```
Query Match      15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 55;
Matches 10: Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

Qy 61 GCTGATGTCCTGTCAAG 77
||:|:|:|:|
Db 1 GCUGGUGUGCUGGCAAG 17

```

RESULT 80
US-10-138-674-8872/c
; Sequence 8872, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for
; TITLE OF INVENTION: Levels of Vascular E
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8872
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-8872

```

```
Query Match      15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 55;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 60 AGCTGATGTCCTGTCAA 76
|||
Db 17 AGTGTGCTGTCTGTCAA 1

```

RESULT 81
US-10-287-949A-8872/c
; Sequence 8872, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggan, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for
; TITLE OF INVENTION: Levels of Vascular Endothelial
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8872
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-8872

```

Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 55;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 60 AGCTGATGTCCTGTCAA 76
Db 17 AGTTGCTGCTTGTCAA 1

```

RESULT 82
US-10-712-633-4058/c
; Sequence 4058, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MOLECULES
; TITLE OF INVENTION: RECEPTOR FOR THE THERAPEUTIC
; FILE REFERENCE: MBH002-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4058
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-712-633-4058

```

Query Match	15.8%	Score 12.2;	DB 1;	Length 17;
Best Local Similarity	82.4%	Pred. No. 55;		
Matches 14: Conservative	0;	Mismatches	3;	Indels 0;
Matches 14: Gaps	0;			

Qy 60 AGCTGATGTCTGTCAA 76
||| ||| ||| ||| ||| ||| ||| |||
Db 17 AGTTGCTGTCTTGTCAA 1

RESULT 83
US-10-913-280-108
Sequence 108, Application US/10913280
Publication No. US2005008984A1
GENERAL INFORMATION:
APPLICANT: Gings, Edward I.
APPLICANT: Galdzicka, Marzena
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES
FILE REFERENCE: 07917-238001
CURRENT APPLICATION NUMBER: US/10/913,280
CURRENT FILING DATE: 2004-08-06
PRIOR APPLICATION NUMBER: US 60/493,238
PRIOR FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: US 60/568,958
PRIOR FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 920

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Primer
US-10-913-280-108
```

```
Query Match      15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 55;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 25 ACTCTGGAGTCCTCTGA 41
Db 1 ACACAGGCGTCTCTGA 17
```

RESULT 84

```
US-10-776-934-113
; Sequence 113, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 113
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-776-934-113
```

```
Query Match      15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15
```

RESULT 85

```
US-10-776-934-592
; Sequence 592, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
```

```
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 592
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorothioate linkage
US-10-776-934-592
```

```
Query Match      15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15
```

RESULT 86

```
US-10-776-934-593
; Sequence 593, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURUE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 593
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: Synthetic oligonucleotide
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (13)..(15)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorothioate linkage
US-10-776-934-593
```

```
Query Match      15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
```

```
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15

RESULT 87
US-10-776-934-594
; Sequence 594, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURIE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 594
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: modified base
; LOCATION: (1)..(4)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (13)..(16)
; OTHER INFORMATION: beta-D-oxy-LNA modified base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)..(13)
; OTHER INFORMATION: phosphorothioate linkage
US-10-776-934-594

Query Match 15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15

RESULT 88
US-10-776-934-595
; Sequence 595, Application US/10776934
; Publication No. US20050014712A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, BO
; APPLICANT: THURIE, CHARLOTTE ALBAEK
; APPLICANT: WESTERGAARD, MAJKEN
; APPLICANT: PETERSEN, KAMILLE DUMONG
; APPLICANT: WISSENBACH, MARGIT
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: 58610(71432)
; CURRENT APPLICATION NUMBER: US/10/776,934
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 60/446,372
; PRIOR FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/523,591
```

```
; PRIOR FILING DATE: 2003-11-19
; NUMBER OF SEQ ID NOS: 741
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 595
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(16)
; OTHER INFORMATION: phosphorothioate linkage
US-10-776-934-595

Query Match 15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64
Db 4 CCAGCGAAGCTG 15

RESULT 89
US-09-866-108-10022
; Sequence 10022, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10022
```


; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-10022

Query Match 15.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCCTC 38
|||||
Db 6 TCTGGAGTCCTC 17

RESULT 90

US-10-723-361-10022
; Sequence 10022, Application US/10723361
; Publication No. US20040137589A1

GENERAL INFORMATION:

; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark

; TITLE OF INVENTION: HUMAN MYOSIN-LIKE POLYPEPTIDE EXPRESSED PREDOMINANTLY IN HEART AN

; FILE REFERENCE: PB0105

; CURRENT APPLICATION NUMBER: US/10/723,361

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: US 09/866,108

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 15755

; SOFTWARE: Acomica Sequence Listing Engine

; SEQ ID NO 10022

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-723-361-10022

Query Match 15.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCCTC 38
|||||
Db 6 TCTGGAGTCCTC 17

RESULT 91

US-10-138-674-6986/c

; Sequence 6986, Application US/10138674

; Publication No. US20040077565A1

GENERAL INFORMATION:

; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MEHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6986
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-6986

Query Match 15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 52 GCCAGCGAAGCTGAT 66
|||||
Db 16 GCCAGCATAGCTGAT 2

RESULT 92

US-10-287-949A-6986/c

; Sequence 6986, Application US/10287949A

; Publication No. US20040102389A1

GENERAL INFORMATION:

; APPLICANT: Ribozyne Pharmaceuticals, Inc.

; APPLICANT: Pavco, Pam

; APPLICANT: McSwiggen, Jim

; APPLICANT: Stinchcomb, Dan

; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re

; FILE REFERENCE: MEHB00-876-N (400/049)

; CURRENT APPLICATION NUMBER: US/10/287,949A

; CURRENT FILING DATE: 2003-04-11

; NUMBER OF SEQ ID NOS: 20822

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6986

; LENGTH: 16

; TYPE: RNA

; ORGANISM: Homo sapiens

US-10-287-949A-6986

Query Match 15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 52 GCCAGCGAAGCTGAT 66
|||||
Db 16 GCCAGCATAGCTGAT 2

RESULT 93

US-10-741-600-73537/c

; Sequence 73537, Application US/10741600

; Publication No. US20050026169A1

GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE REFERENCE: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 73537

```
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-73537

Query Match      15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 55;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 31 GAGTCCTCTGAGAGG 45
Db 16 GAGTCCTCCGGAGG 2

RESULT 94
US-10-257-017B-41787
; Sequence 41787, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 41787
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012525
US-10-257-017B-41787

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAGA 51
Db 1 TGAGAGGTAAGA 13

RESULT 95
US-10-257-017B-41788/c
; Sequence 41788, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 41788
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0012525
US-10-257-017B-41788

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 43;
```

```
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAGA 51
Db 13 TGAGAGGTAAGA 1

RESULT 96
US-10-257-017B-184441
; Sequence 184441, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 184441
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045516
US-10-257-017B-184441

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAGA 51
Db 1 TGAGATGTAAGA 13

RESULT 97
US-10-257-017B-184442/c
; Sequence 184442, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 184442
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0045516
US-10-257-017B-184442

Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAGA 51
Db 13 TGAGATGTAAGA 1
```

```

RESULT 98
US-10-142-729-26/c
; Sequence 26, Application US/10142729
; Publication No. US20030165888A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
; FILE REFERENCE: OASBIO.005A
; CURRENT APPLICATION NUMBER: US/10/142,729
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-142-729-26

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 99
US-10-142-729-39/c
; Sequence 39, Application US/10142729
; Publication No. US20030165888A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
; FILE REFERENCE: OASBIO.005A
; CURRENT APPLICATION NUMBER: US/10/142,729
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-142-729-39

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 100
US-10-375-504-26/c
; Sequence 26, Application US/10375504
; Publication No. US20030170711A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
; FILE REFERENCE: OASBIO.005C1
; CURRENT APPLICATION NUMBER: US/10/375,504
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 10/142,729
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-375-504-26

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 101
US-10-375-504-39/c
; Sequence 39, Application US/10375504
; Publication No. US20030170711A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
; FILE REFERENCE: OASBIO.005C1
; CURRENT APPLICATION NUMBER: US/10/375,504
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 10/142,729
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-142-729-39

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Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 100
US-10-375-504-26/c
; Sequence 26, Application US/10375504
; Publication No. US20030170711A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
; FILE REFERENCE: OASBIO.005C1
; CURRENT APPLICATION NUMBER: US/10/375,504
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 10/142,729
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-375-504-26

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1

RESULT 101
US-10-375-504-39/c
; Sequence 39, Application US/10375504
; Publication No. US20030170711A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Bob D.
; APPLICANT: Riley, Timothy A.
; TITLE OF INVENTION: OLIGONUCLEOTIDE PROBES AND PRIMERS
; TITLE OF INVENTION: COMPRISING UNIVERSAL BASES FOR DIAGNOSTIC PURPOSES
; FILE REFERENCE: OASBIO.005C1
; CURRENT APPLICATION NUMBER: US/10/375,504
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 10/142,729
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: 60/306,229
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/136,080
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/060,673
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-375-504-39

```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4, 10
; OTHER INFORMATION: n = modified base
US-10-375-504-39

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 80.0%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 19 GATCAACTCTGGAG 33
Db 15 GATACNGCTCTNGAG 1
||||| |||||

RESULT 102
US-10-719-993-55182
; Sequence 55182, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 55182
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-55182

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 CCTGGGGGATACAA 25
Db 1 CCGGGGGGATACAA 13
||||| |||||

RESULT 103
US-09-875-453-65/c
; Sequence 65, Application US/09875453
; Publication No. US20030027320A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruce, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 4600-0135-30
; CURRENT APPLICATION NUMBER: US/09/875,453
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453-65

Query Match      14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 65;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAAGAGC 53
Db 16 CTGGGAGGTGGAGAGC 1
||||| |||||

RESULT 104
US-10-331-907-450
; Sequence 450, Application US/10331907
; Publication No. US20030181660A1
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. US20030181660A1el LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA: US/10/331,907
; FILING DATE: 31-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J. Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 450:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 450:
US-10-331-907-450
```

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 65;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAAGAGCC 54
Db 1 TCACAGGTAAAGAGCC 16

RESULT 105

US-10-407-807-67/c
; Sequence 67, Application US/10407807
; Publication No. US20040096848A1
; GENERAL INFORMATION:
; APPLICANT: THRUE, ANJA MOLHART
; APPLICANT: HOG, ANJA MOLHART
; APPLICANT: KRISTJANSEN, PAUL E.G.
; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION HIP-1ALPHA

; FILE REFERENCE: 57390 (45120)
; CURRENT APPLICATION NUMBER: US/10/407,807
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: 60/370,126
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 67
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-407-807-67

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 65;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAGC 62
Db 16 AAACACACAGCGAGC 1

RESULT 106

US-10-450-797-548/c
; Sequence 548, Application US/10450797
; Publication No. US20040142335A1
; GENERAL INFORMATION:
; APPLICANT: Petersohn, Dirk
; APPLICANT: Conradt, Marcus
; APPLICANT: Hofmann, Kay
; TITLE OF INVENTION: METHOD FOR DETERMINING SKIN STRESS OR SKIN AGEING IN VITRO

; FILE REFERENCE: HENK-0041
; CURRENT APPLICATION NUMBER: US/10/450,797
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/EP01/15178
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: DE 101 00 121.5
; PRIOR FILING DATE: 2001-01-03
; NUMBER OF SEQ ID NOS: 1435
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 548
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-450-797-548

Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATACAACTCTG 30
Db 11 ATACAACTCTG 1

RESULT 107

US-10-257-017B-320928/c
; Sequence 320928, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 320928
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0029975

US-10-257-017B-320928

Query Match 14.3%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GAGAGGTAAAG 50
Db 12 GAGAGGTAAAG 2

RESULT 108

US-10-257-017B-14593
; Sequence 14593, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:

; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14593
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003290

US-10-257-017B-14593

Query Match 14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 41 AGAGGTAAAGAGC 53
Db 1 AGAAGTAAAGAGY 13

RESULT 109

US-10-257-017B-14594/c

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; Sequence 14594, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 14594
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0003290
US-10-257-017B-14594

Query Match      14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGAGC 53
Db 13 AGAAGTAAAGAGY 1

RESULT 110
US-10-257-017B-181997
; Sequence 181997, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 181997
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044987
US-10-257-017B-181997

Query Match      14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAG 49
Db 2 TGAGAGGTAAAG 12

RESULT 111
US-10-257-017B-181998/c
; Sequence 181998, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
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; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 181998
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0044987
US-10-257-017B-181998

Query Match      14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAG 49
Db 12 TGAGAGGTAAAG 2

RESULT 112
US-10-257-017B-224917
; Sequence 224917, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 224917
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054826
US-10-257-017B-224917

Query Match      14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGAG 51
Db 2 AGAGGTAAAGAG 12

RESULT 113
US-10-257-017B-224918/c
; Sequence 224918, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
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; SEQ ID NO 224918
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0054826
US-10-257-017B-224918

Query Match          14.3%; Score 11; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTAAGA 51
DB 12 AGAGGTAAGA 2

RESULT 114
US-09-998-027-20
; Sequence 20, Application US/09998027
; Publication No. US20030093819A1
; GENERAL INFORMATION:
; APPLICANT: D'Andrea et al.
; TITLE OF INVENTION: Methods and Compositions for the
; TITLE OF INVENTION: Diagnosis and Treatment of Cancers Associated with Defective
; TITLE OF INVENTION: DNA Repair Mechanisms
; FILE REFERENCE: 2486/101
; CURRENT APPLICATION NUMBER: US/09/998,027
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; OTHER INFORMATION: Intron/Exon Junctions of FANCD
US-09-998-027-20

Query Match          14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AGGTAAGAGC 53
DB 2 AGGTAAGAGC 12

RESULT 115
US-10-165-099-20
; Sequence 20, Application US/10165099
; Publication No. US20030188326A1
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS OF CANCER SUSCEPTIBILITY
; TITLE OF INVENTION: DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THEREOF
; FILE REFERENCE: 7032/2055
; CURRENT APPLICATION NUMBER: US/10/165,099
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 09/998,027
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/245,756
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-165-099-20

Query Match          14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 55;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AGGTAAGAGC 53
DB 2 AGGTAAGAGC 12

RESULT 116
US-09-504-231A-1179/c
; Sequence 1178, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: TPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1178
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1178

Query Match          14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GTAAGAGGCCA 55
DB 13 GTAAGAGGCCA 3

RESULT 117
US-09-504-231A-1179/c
; Sequence 1179, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: TPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1179

Query Match          14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GTAAAGAGCCA 55
Db      11 GTAAAGAGCCA 1
|||||

RESULT 118
US-09-274-553D-1178/c
; Sequence 1178, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: TPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1178
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1178

Query Match          14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GTAAAGAGCCA 55
Db      13 GTAAAGAGCCA 3
|||||

RESULT 119
US-09-274-553D-1179/c
; Sequence 1179, Application US/09274553D
; Patent No. US20020082225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE
; FILE REFERENCE: TPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1179
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1179

Query Match          14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GTAAAGAGCCA 55
Db      11 GTAAAGAGCCA 1
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Search completed: April 19, 2006, 16:13:31
Job time : 0.001 secs
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 16:15:43 ; Search time 0.001 Seconds
(without alignments)
1028.104 Million cell updates/sec

Title: US-10-643-038-17_994-1070

Perfect score: 77

Sequence: 1 caaacagacggcctgggga.....gaagctgagtctctgtcaag 77

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 351 seqs, 6676 residues

Total number of hits satisfying chosen parameters: 702

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 351 summaries

Database : pubnewdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 3	17.4	22.6	19	US-11-101-244-512380 Sequence 512380, A
C 4	17.4	22.6	19	US-11-083-784-512380 Sequence 512380, A
C 5	16.4	21.3	19	US-11-101-244-1197318 Sequence 1197318, A
C 6	16.4	21.3	19	US-11-101-244-1197383 Sequence 1197383, A
C 7	16.4	21.3	19	US-11-083-784-1197318 Sequence 1197318, A
C 8	16.4	21.3	19	US-11-083-784-1197383 Sequence 1197383, A
C 9	16.4	21.3	22	US-10-310-914A-1373610 Sequence 1373610, A
C 10	16.2	21.0	21	US-10-310-914A-99908 Sequence 99908, A
C 11	16.2	21.0	23	US-10-310-914A-591217 Sequence 591217, A
C 12	16.2	21.0	23	US-10-310-914A-921349 Sequence 921349, A
C 13	15.8	20.5	21	US-10-972-767-181 Sequence 181, App
C 14	15.8	20.5	22	US-11-069-908-3819 Sequence 3819, App
C 15	15.6	20.3	22	US-10-310-914A-1094322 Sequence 1094322, A
C 16	15.4	20.0	19	US-11-101-244-826612 Sequence 826612, A
C 17	15.4	20.0	19	US-11-101-244-1197334 Sequence 1197334, A
C 18	15.4	20.0	19	US-11-101-244-1197395 Sequence 1197395, A
C 19	15.4	20.0	19	US-11-101-244-1375618 Sequence 1375618, A
C 20	15.4	20.0	19	US-11-083-784-826612 Sequence 826612, A
C 21	15.4	20.0	19	US-11-083-784-1197334 Sequence 1197334, A
C 22	15.4	20.0	19	US-11-083-784-1197395 Sequence 1197395, A
C 23	15.4	20.0	19	US-11-083-784-1375618 Sequence 1375618, A
C 24	15.4	20.0	21	US-10-310-914A-1373632 Sequence 1373632, A
C 25	15.2	19.7	20	US-10-310-914A-820857 Sequence 820857, A
C 26	15.2	19.7	21	US-10-310-914A-945704 Sequence 945704, A
C 27	15.2	19.7	21	US-10-310-914A-1213419 Sequence 1213419, A
C 28	14.8	19.2	18	US-10-310-914A-45021 Sequence 45021, A
C 29	14.8	19.2	18	US-10-310-914A-921346 Sequence 921346, A
C 30	14.8	19.2	18	US-10-310-914A-946718 Sequence 946718, A
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1	US-11-101-244-686504	19	19.2	14.8	35	Sequence 686504, A
1	US-11-101-244-716743	19	19.2	14.8	36	Sequence 716743, A
1	US-11-101-244-741998	19	19.2	14.8	37	Sequence 741998, A
1	US-11-101-244-1221841	19	19.2	14.8	38	Sequence 1221841, A
1	US-11-101-244-1221940	19	19.2	14.8	39	Sequence 1221940, A
1	US-11-101-244-1222038	19	19.2	14.8	40	Sequence 1222038, A
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1	US-11-083-784-741998	19	19.2	14.8	46	Sequence 741998, A
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1	US-11-083-784-1221940	19	19.2	14.8	48	Sequence 1221940, A
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1	US-11-101-244-1256070	19	18.7	14.4	56	Sequence 1256070, A
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1	US-11-101-244-1435551	19	18.7	14.4	58	Sequence 1435551, A
1	US-11-101-244-1526025	19	18.7	14.4	59	Sequence 1526025, A
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1	US-11-101-244-931449	19	18.4	14.2	84	Sequence 931449, A
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1	US-11-101-244-1286557	19	18.4	14.2	89	Sequence 1286557, A
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1	US-11-083-784-404601	19	18.4	14.2	94	Sequence 404601, A
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1	US-11-083-784-716725	19	18.4	14.2	99	Sequence 716725, A
1	US-11-083-784-749629	19	18.4	14.2	100	Sequence 749629, A
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ALIGNMENTS

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; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
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Query Match 23.6%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 27 TCTGGAGTCTCTGAGAGGTAAA 49
|||

```

```

Db 24 TCAGGAGTCTCTTGGAGGTAAA 2
|||

```

RESULT 2

```

US-11-121-849-18534/c
; Sequence 18534, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949

```

```
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18534
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-18534
```

```
Query Match      22.9%; Score 17.6; DB 1; Length 25;
Best Local Similarity 93.3%; Pred. No. 41;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 29 TGGAGTCTCTGAGAGGTAAGAG 52
Db 24 TGGAGTAATCTGAGGGTAAGAG 1
```

RESULT 3

```
US-11-101-244-512380/c
; Sequence 512380, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 512380
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-512380
```

```
Query Match      22.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 23 CAACTCTGGAGTCTCTCTGA 41
Db 19 CAACACTGGAGTCTCTCTGA 1
```

RESULT 4

```
US-11-083-784-512380/c
; Sequence 512380, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
```

```
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 512380
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-512380
```

```
Query Match      22.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 23 CAACTCTGGAGTCTCTCTGA 41
Db 19 CAACACTGGAGTCTCTCTGA 1
```

RESULT 5

```
US-11-101-244-1197318
; Sequence 1197318, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197318
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1197318
```

```
Query Match      21.3%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 58 GAAGCTGATGTCCTCTGTCA 75
Db 2 GAAGCUGUGUCCUGUCA 19
```

RESULT 6

```
US-11-101-244-1197383
; Sequence 1197383, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
```

; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197383
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1197383

Query Match 21.3%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGCTCTGTCA 75
|||||:|:|:|:|:
Db 2 GAAGCUGUGUCCUGUCA 19

RESULT 7

US-11-083-784-1197318
; Sequence 1197318, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197318
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1197318

Query Match 21.3%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGCTCTGTCA 75
|||||:|:|:|:|:
Db 2 GAAGCUGUGUCCUGUCA 19

RESULT 8

US-11-083-784-1197383
; Sequence 1197383, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197383
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1197383

Query Match 21.3%; Score 16.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGCTCTGTCA 75
|||||:|:|:|:|:
Db 2 GAAGCUGUGUCCUGUCA 19

RESULT 9

US-10-310-914A-1373610/c
; Sequence 1373610, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1373610
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1373610

Query Match 21.3%; Score 16.4; DB 1; Length 22;
Best Local Similarity 94.4%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCTCTGTGAG 44
|||||:|:|:|:|:
Db 18 TCTGGAGTCTCTGTGAG 1

RESULT 10

US-10-310-914A-99908/c
; Sequence 99908, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99908
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-99908

Query Match 21.0%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 31 GAGTCTCTGAGAGGTAAAGA 51
||| ||| ||| ||| ||| ||| ||| |||
Db 21 GAGTCTTCTGAGAGCTAAGGA 1

```

RESULT 11
US-10-310-914A-591217
; Sequence 591217, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Krizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 591217
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-591217

```

Query Match	21.0%	Score 16.2;	DB 1;	Length 23;
Best Local Similarity	76.2%;	Pred. No. 65;		
Matches 16;	Conservative	2;	Mismatches 3;	Indels 0;
Gaps	0;			

```

Qy      31  GAGTCCTCTGAGAGGTAAGA 51
      |||||
Db      21  GAGTCCTCTGAGAGCTAAGGA 1
      |||||

RESULT 11
US-10-310-914A-591217
; Sequence 591217, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 591217
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-591217

```

```

Query Match      21.0%; Score 16.2; DB 1; Length 23;
Best Local Similarity 76.2%; Pred. NO. 65;
Matches 16; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      8 GAGGGCCTGGGGATACAACTC 28
      |||||:|||||
Db       3 GAAGGGCUGGGGACACAACTC 23

RESULT 13
US-10-972-767-181
; Sequence 181, Application US/10972767
; Publication No. US20060008815A1
; GENERAL INFORMATION:
; APPLICANT: METAMORPHIX, INC.
; APPLICANT: Rosenfeld, David
; APPLICANT: Kerr, Richard
; APPLICANT: Hutton, Michelle

```

```
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1094322
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1094322

Query Match      20.3%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 80;
Matches 18; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

Qy 11 GCCTGGGGATACAACTCTGGA 32
Db 22 GCCCTGGGGATCCAGCCCTGGA 1

RESULT 16
US-11-101-244-826612/c
; Sequence 826612, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 826612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-826612

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 59 AAGCTGATGTCCTGTCA 75
Db 17 AAGCTGATGTCCTGTCA 1

RESULT 17
US-11-101-244-1197334
; Sequence 1197334, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 826612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-826612

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy 59 AAGCTGATGTCCTGTCA 75
Db 17 AAGCTGATGTCCTGTCA 1

RESULT 18
US-11-101-244-1197395
; Sequence 1197395, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197395
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1197395

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCTGTCA 75
Db 1 AAGCTGUGUGUCUGUCA 17

RESULT 19
US-11-101-244-1375618
; Sequence 1375618, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1197395
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1375618

Query Match      20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCTGTCA 75
Db 1 AAGCTGUGUGUCUGUCA 17
```


; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1375618
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1375618

Query Match 20.0%; Score 15.4; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 98;
Matches 11; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCTCTCGAGA 43
:|||||:|:|:|
Db 3 UCUGGAGUCCUCUGUGA 19

RESULT 24
US-10-310-914A-1373632/c
; Sequence 1373632, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1373632
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1373632

Query Match 20.0%; Score 15.4; DB 1; Length 21;
Best Local Similarity 94.1%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCTCTCGAGA 43
|||||:|:|:|
Db 17 TCTGGAGTCTCTGTGA 1

RESULT 25
US-10-310-914A-820857
; Sequence 820857, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 820857
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-820857

Query Match 19.7%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 42 GAGGTAAGAGCCAGCGAAG 61
|||||:|:|:|
Db 1 GAGGTAAGAGCCAGCGAAG 20

RESULT 26
US-10-310-914A-946704/c
; Sequence 946704, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 946704
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-946704

Query Match 19.7%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 42 GAGGTAAGAGCCAGCGAAG 61
|||||:|:|:|
Db 20 GAGGAGAGAGCCAGCGAG 1

RESULT 27
US-10-310-914A-1213419
; Sequence 1213419, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1213419
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1213419

Query Match 19.5%; Score 15; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 10; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCTCTG 40
:|:|:|:|:|:|
Db 2 CUCUGGAGUCCUCUG 16

RESULT 28
US-10-310-914A-45021
; Sequence 45021, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac

```
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45021
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-45021

Query Match      19.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.2e+02;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGCCTGGGGATACAATC 28
|||:||||:||||:
Db 1 GGCCTGGGGATACAATC 18

RESULT 29
US-10-310-914A-921346
; Sequence 921346, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 921346
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-921346

Query Match      19.2%; Score 14.8; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGCCTGGGGATACAATC 28
|||:||||:||||:
Db 1 GGCCTGGGGATACAATC 18

RESULT 30
US-10-310-914A-946718/c
; Sequence 946718, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 946718
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-946718

Query Match      19.2%; Score 14.8; DB 1; Length 18;
```

```
Best Local Similarity 88.9%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 42 GAGGTAAAGAGCCAGCGA 59
|||||:|||||:|||||
Db 18 GAGGTAAAGAGCCAGCGA 1

RESULT 31
US-10-310-914A-1358783/c
; Sequence 1358783, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1358783
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1358783

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAGCTG 64
|||||:|||||:|||||
Db 18 AAAGAGCCAGCGAAGCTG 1

RESULT 32
US-11-101-244-446294/c
; Sequence 446294, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 446294
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-446294

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 CTCCTGGAGTCCTCTGAGA 43
|||||:|||||:|||||
Db 18 CTCCTGGAGTCCTCTGATA 1
```

RESULT 33

US-11-101-244-462186
 ; Sequence 462186, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 462186
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-462186

Query Match 19.2%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 21 TACAACCTGGAGTCCTC 38
 :||||| |:|||||:|
 Db 2 UACAACACUGGAGUCAUC 19

RESULT 34

US-11-101-244-673763
 ; Sequence 673763, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 673763
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-673763

Query Match 19.2%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 61.1%; Pred. No. 1.1e+02;
 Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 60 AGCTGATGTCCTGTCAAG 77
 ||||| |:|:|:|
 Db 2 AGCUGUGUUCUGUCAAG 19

RESULT 35

US-11-101-244-673763

US-11-101-244-686604
 ; Sequence 686604, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 686604
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-686604

Query Match 19.2%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 47 AAAGAGCCGAGGAGCTG 64
 ||||| |||||:|
 Db 2 AAAGAGCCGAGGAGCAUG 19

RESULT 36

US-11-101-244-716743/C
 ; Sequence 716743, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 716743
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-716743

Query Match 19.2%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 25 ACTCTGGAGTCCTCTGAG 42
 ||||| |||||
 Db 19 ACTCTGGAGTCCTCTGAG 2

RESULT 37

US-11-101-244-741998

```
; Sequence 741998, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 741998
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-741998

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 42 GAGTAAAGAGCCAGCGA 59
   ||||| ||||| |||||
Db 2 GAGGUAAGGCGCCAGUGA 19

RESULT 38
US-11-101-244-1221841
; Sequence 1221841, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1221841
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1221841

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTGATGTCCT 71
   ||| ||||| :|||
Db 1 CAGAGAAGCTGCGUGCCU 18

RESULT 40
US-11-101-244-1222038
; Sequence 1222038, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1222038
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1222038

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTGATGTCCT 71
   ||| ||||| :|||
Db 1 CAGAGAAGCTGCGUGCCU 18

RESULT 41
US-11-083-784-446294/c
; Sequence 446294, Application US/11083784
; Publication No. US20050245475A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 446294
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-446294

```

```

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 26 CTCGGAGTCTCTGACA 43
Db 18 CTCGGAGTCTCTGATA 1

```

RESULT 42

```

US-11-083-784-462186
; Sequence 462186, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 462186
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-462186

```

```

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 21 TACAACCTCTGGAGTCCTC 38
Db 2 UACAACACUGGAGUCAUC 19

```

RESULT 43

```

US-11-083-784-673763
; Sequence 673763, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 673763
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-673763

```

```

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 61.1%; Pred. No. 1.1e+02;
Matches 11; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 60 AGCTGATGTCCTGCAAG 77
Db 2 AGCUGGUGUCUGUCAAG 19

```

RESULT 44

```

US-11-083-784-686604
; Sequence 686604, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 686604
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-686604

```

```

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 47 AAGAGCCGCGAGCTG 64
Db 2 AAGAGCCGCGAACAUG 19

```

```
RESULT 45
US-11-083-784-716743/C
; Sequence 716743, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 716743
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-716743

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTCCTGTGAG 42
Db      19 ACTCTGGACTCCTGTGAG 2

RESULT 46
US-11-083-784-741998
; Sequence 741998, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 741998
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-741998

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      42 GAGGTAAGAGCCAGCGA 59
Db      2 GAGGTAAGAGCCAGUGA 19

RESULT 47
US-11-083-784-1221841
; Sequence 1221841, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1221841
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1221841

Query Match      19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      54 CAGCGAAGCTGATGTCCT 71
Db      1 CAGAGAAGCGUGUGCCU 18

RESULT 48
US-11-083-784-1221940
; Sequence 1221940, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1221940
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1221940

Query Match      19.2%; Score 14.8; DB 1; Length 19;
```

Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 54 CAGCGAGCTGATCTCT 71
||| |||||:|:|:|:
Db 1 CAGAGAAGCUGCUGCCU 18

RESULT 49

US-11-083-784-1222038
; Sequence 1222038, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1222038
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens

US-11-083-784-1222038

Query Match 19.2%; Score 14.8; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 54 CAGCGAGCTGATCTCT 71
||| |||||:|:|:|:
Db 1 CAGAGAAGCUGCUGCCU 18

RESULT 50

US-10-310-914A-1045625/c
; Sequence 1045625, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and

; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1045625
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1045625

Query Match 19.2%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 15 TGGGGATACCACTCTGCA 32
|||||||:|:|:|:
Db 19 TGGGGATACCACTCTGCA 2

RESULT 51

US-10-310-914A-144915/c
; Sequence 144915, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvizat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 144915
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-144915

Query Match 18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 ACAAGAGCGCTGGG 19
|||||:|:|:|:
Db 18 ACAAGAGCGCTGGG 3

RESULT 52

US-11-101-244-527885/c
; Sequence 527885, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527885
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-527885

Query Match 18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATCTCTGT 73
|||||:|:|:|:
Db 18 GAATCTGATCTCTGT 3

RESULT 53

US-11-101-244-681299
; Sequence 681299, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmaco, Inc.

; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1323244
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-1323244

Query Match 18.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 68.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCTCTGAGA 43
 Db 2 CUGGACUCCUCUGAGA 17

RESULT 58
 US-11-101-244-1435551/c
 ; Sequence 1435551, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1435551
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-1435551

Query Match 18.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCTCTGAG 42
 Db 17 TCTGGAGACCTCTGAG 2

RESULT 59
 US-11-101-244-1526025/c
 ; Sequence 1526025, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1526025
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-1526025

Query Match 18.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCGGAGTCTCTGGA 41
 Db 16 CTCGGAGTACTCTGA 1

RESULT 60
 US-11-101-244-1526053/c
 ; Sequence 1526053, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1526053
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-1526053

Query Match 18.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 26 CTCGGAGTCTCTGGA 41
 Db 18 CTCGGAGTACTCTGA 3

RESULT 61
 US-11-083-784-527885/c
 ; Sequence 527885, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527885
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-527885
```

```
Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      58 GAAGCTGATGTCCTGT 73
Db      18 GAATCTGATGTCCTGT 3
```

RESULT 62

```
US-11-083-784-681299
; Sequence 681299, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 681299
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-681299
```

```
Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      22 ACAACTCTGGAGTCCT 37
Db      3 ACAACACUGGAGUCCU 18
```

RESULT 63

```
US-11-083-784-1025484/c
; Sequence 1025484, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```

```
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1025484
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1025484
```

```
Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      58 GAAGCTGATGTCCTGT 73
Db      18 GAAGCAGATGTCCTGT 3
```

RESULT 64

```
US-11-083-784-1155118
; Sequence 1155118, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1155118
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1155118
```

```
Query Match      18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 68.8%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      22 ACAACTCTGGAGTCCT 37
Db      3 ACAACUCUGGUGUCCU 18
```

RESULT 65

```
US-11-083-784-1256070/c
; Sequence 1256070, Application US/11083784
; Publication No. US20050245475A1
```

; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: US/10/714,333
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1256070
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-1256070

Query Match 18.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAGC 62
 DB 18 AAAGAGCCAGTGAAGC 3

RESULT 66

US-11-083-784-1323244
 ; Sequence 1323244, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: US/10/714,333
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1323244
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-1323244

Query Match 18.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 68.8%; Pred. No. 1.3e+02;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGAGTCTCTGAGA 43
 DB 2 CUGGACUCCUGAGA 17

RESULT 67

Query Match 18.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 CTCTGGAGTCTCTGA 41
 DB 16 CTCTGGAGTCTCTGA 1

US-11-083-784-1435551/c
 ; Sequence 1435551, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: US/10/714,333
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1435551
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-1435551

Query Match 18.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42
 DB 17 TCTGGAGACCTCTGAG 2

RESULT 68

US-11-083-784-1526025/c
 ; Sequence 1526025, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: US/10/714,333
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1526025
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-1526025

Query Match 18.7%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 1.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 69
US-11-083-784-1526053/c
; Sequence 1526053, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13498US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 159111
; SOFTWARE: Proprietary
; SEQ ID NO 1526053
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1526053

Query Match 18.7%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 CTCTGGAGTCTCTGA 41
|||||
Db 18 CTCTGGAGTCTCTGA 3

RESULT 70
US-10-750-185-15591/c
; Sequence 15591, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15591
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-750-185-15591

Query Match 18.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 AACTCTGGAGTCTCT 39
|||||
Db 20 AACTCTGGAGTCTCT 5

RESULT 71
US-10-750-623-15591/c
; Sequence 15591, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15591
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-750-623-15591

Query Match 18.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 AACTCTGGAGTCTCT 39
|||||
Db 20 AACTCTGGAGTCTCT 5

RESULT 72
US-10-310-914A-562241/c
; Sequence 562241, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 562241
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-562241

Query Match 18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 35 CCTCTGAGAGTTAAAGAC 53
|||||
Db 19 CCGCTGAGTGCACAAAGAC 1

RESULT 73
US-10-310-914A-1111642/c
; Sequence 1111642, Application US/10310914A

|||||
Db 20 AACTCTGGAGTCTCT 5

RESULT 71
US-10-750-623-15591/c
; Sequence 15591, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15591
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-750-623-15591

Query Match 18.7%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 24 AACTCTGGAGTCTCT 39
|||||
Db 20 AACTCTGGAGTCTCT 5

RESULT 72
US-10-310-914A-562241/c
; Sequence 562241, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 562241
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-562241

Query Match 18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 35 CCTCTGAGAGTTAAAGAC 53
|||||
Db 19 CCGCTGAGTGCACAAAGAC 1

RESULT 73
US-10-310-914A-1111642/c
; Sequence 1111642, Application US/10310914A

```

; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1111642
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1111642

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 25 ACTCTGGAGTCTCTGAGA 43
   ||||| ||||| |||||
Db 19 ACCCTGGACCTCTGAGA 1

RESULT 74
US-11-101-244-197226
; Sequence 197226, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 197226
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-197226

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAGCTGATGT 68
   ||||| ||||| ||||| |||||
Db 1 GGGCCAGGUNGCGUGUGU 19

RESULT 75
US-11-101-244-404601/c
; Sequence 404601, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 404601
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-404601

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGTCC 36
   ||||| ||||| |||||
Db 19 GAATACAAATCTGGAATCC 1

RESULT 76
US-11-101-244-518286/c
; Sequence 518286, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 518286
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-518286

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 20 ATACAACTCTGGAGTCTC 38
   ||||| ||||| |||||
Db 19 ATACAACTCTGCTCTCCTC 1

RESULT 77
US-11-101-244-527824/c
; Sequence 527824, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

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; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527824
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-527824

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 AGCCAGCGAAGCTGATGTC 69
Db 19 AACCATGTAATCTGATGTC 1

RESULT 78
US-11-101-244-539604
; Sequence 539604, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 539604
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-539604

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 42 GAGCTAAGAGCCAGCGAA 60
Db 1 GAGGUAAGACUCACGCUA 19

RESULT 79
US-11-101-244-618922
; Sequence 618922, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 618922
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-618922

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 25 ACTCTGGAGTCCTCTGAGA 43
Db 1 AAUCUUGAGUCUCUGAGA 19

RESULT 80
US-11-101-244-716725/c
; Sequence 716725, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 716725
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-716725

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCCTCTGGA 41
Db 19 CTACTCTGGACTCTCTGTGA 1

RESULT 81
US-11-101-244-749629/c
; Sequence 749629, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349905
; CURRENT APPLICATION NUMBER: US/11/101,244
```

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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 749629
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-749629

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGGTTAAAGAG 52
Db 19 TCCTCTTAGAGGTACAGAG 1

RESULT 82
US-11-101-244-819751
; Sequence 819751, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 819751
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-819751

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 30 GGAGTCTCTGAGAGGTAA 48
Db 1 GGAGAGUCUGAGAGGUA 19

RESULT 83
US-11-101-244-840452
; Sequence 840452, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

; CURRENT APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 840452
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-840452

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 42 GAGGTAAGAGCCGAGCGAA 60
Db 1 GAGGTAAGAGCCGAGGAA 19

RESULT 84
US-11-101-244-931449
; Sequence 931449, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 931449
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-931449

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 47 AAAGAGCCGAGCGAAGCTGA 65
Db 1 AAAGAGCCCAUCCAGGCUAA 19

RESULT 85
US-11-101-244-1006983/c
; Sequence 1006983, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
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; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1006983
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1006983

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTGA 41
Db 19 CAAATCTGGAGTCTCTTA 1

RESULT 86
US-11-101-244-1178034/c
; Sequence 1178034, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1178034
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1178034

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAACAGACGGCTGGG 19
Db 19 CAATCATGACGGCTGGT 1

RESULT 87
US-11-101-244-1238798
; Sequence 1238798, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1238798
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1238798

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTGA 41
Db 19 CATCTCTGGAGTCAGCTGA 1

RESULT 88
US-11-101-244-1257649/c
; Sequence 1257649, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1257649
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1257649

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCTCTGA 41
Db 19 CATCTCTGGAGTCAGCTGA 1

RESULT 89
US-11-101-244-1286557/c
; Sequence 1286557, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286557
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1286557
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; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286557
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1286557

Query Match      18.4%  Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%  Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  56 GCGAAGCTGATGTCCTGTC 74
Db  19 GTGAAGATGAAGTCTCTGC 1

RESULT 90
US-11-101-244-1327450/c
; Sequence 1327450, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327450
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1327450

Query Match      18.4%  Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%  Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  54 CAGCGAAGCTGATGTCCTG 72
Db  19 CAATGAAGCTGAGGTCCTG 1

RESULT 91
US-11-101-244-1402806/c
; Sequence 1402806, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
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; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1402806
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1402806

Query Match      18.4%  Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%  Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  23 CAACTCTGGAGTCTCTGA 41
Db  19 CAAATCTGAATCTCTGA 1

RESULT 92
US-11-101-244-1508424/c
; Sequence 1508424, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1508424
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1508424

Query Match      18.4%  Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%  Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  34 TCCTCTGAGAGGTAAGAG 52
Db  19 TTCTTTGAGAGGTAAGGAG 1

RESULT 93
US-11-083-784-197226
; Sequence 197226, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
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; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 539604
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-539604

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 42 GAGTAAAGCCGAGCGAA 60
    ||||:|||||
Db 1 GAGGUAAGACUCAGCUGAA 19

RESULT 98
US-11-083-784-618922
; Sequence 618922, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 618922
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-618922

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 25 ACTCTGGAGTCCTCTGAGA 43
    |:|:|:|:|:|:|:|
Db 1 AAUCUUGAGUCUUCUGAGA 19

RESULT 99
US-11-083-784-716725/c
; Sequence 716725, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

```

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 716725
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-716725

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 23 CAACCTCGAGTCCTCTGA 41
    |||||:|||||
Db 19 CTACTCTGGACTCCTGTGA 1

RESULT 100
US-11-083-784-749629/c
; Sequence 749629, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 749629
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-749629

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 34 TCCTCTGGAGGTAAGAG 52
    |||||:|||||
Db 19 TCTTCTTAGAGGTACAGAG 1

RESULT 101
US-11-083-784-819751
; Sequence 819751, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 819751
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-819751

Query Match 18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 30 GGAGTCTCTGAGAGGTAA 48
|||||:|||||:
Db 1 GGAGAGCUCGAGAGGUA 19

RESULT 102
US-11-083-784-840452
; Sequence 840452, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 840452
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-840452

Query Match 18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 42 GAGGTAAAGCAGCGCAA 60
|||||:
Db 1 GAGGAAAGCAGCGCAA 19

RESULT 103
US-11-083-784-931449
; Sequence 931449, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 931449
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-931449

Query Match 18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 47 AAAGAGCCAGCGAAGCTGA 65
|||||:
Db 1 AAAGAGCCAUCCAAGCUAA 19

RESULT 104
US-11-083-784-1006983/c
; Sequence 1006983, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1006983
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1006983

Query Match 18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 23 CAACTCTGGAGTCTCTGA 41
|||||:
Db 19 CAAATCTGGAGTCTCTTA 1

RESULT 105
US-11-083-784-1178034/c

```
; Sequence 1178034, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1178034
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1178034

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAACACAGAGCGGCTGGG 19
    |||||:|||||
DB 19 CAATCATGAGCGGCTGGT 1

RESULT 106
US-11-083-784-1238798
; Sequence 1238798, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1238798
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1238798

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 1.3e+02;
Matches 12; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACCTCGAGTCTCTGGA 41
    |||||:|||||:|:|
DB 1 CAACUCUGGUGACUUCUGA 19

RESULT 107
US-11-083-784-1257649/c
; Sequence 1257649, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1257649
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1257649

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACCTCGAGTCTCTGGA 41
    |||||:|||||
DB 19 CATCTCTGGAGTCAGCTGA 1

RESULT 108
US-11-083-784-1286557/c
; Sequence 1286557, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286557
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1286557

Query Match      18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 56 GCGAAGCTGATGTCCTGTC 74
```

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 23 CAACTCTGGAGTCCTCTGA 41
||| ||| | ||| |||
Db 19 CAAATCTGAATTCTCTGA 1

RESULT 111
US-11-083-784-1508424/c
; Sequence 1508424, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1508424
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1508424

Query Match 18.4%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 34 TCCTCTGAGGTAAAGAG 52
||| ||| ||| ||| ||| |||
Db 19 TTCTTTGAGAGTAAAGAG 1

RESULT 112
US-10-310-914A-128507/c
; Sequence 128507, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128507
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-128507

Query Match 18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGACCGCA 59
||||| ||| ||| ||| ||| |||
Db 20 AGAGGGAGAGCGGCGCA 2

```
RESULT 113
US-10-310-914A-658051/c
; Sequence 658051, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 658051
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-658051

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      15 TGGGATACACTCTGGAG 33
Db      20 TGGGATTCAGCTCTAGAG 2

RESULT 114
US-10-310-914A-833580/c
; Sequence 833580, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 833580
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-833580

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      38 CTGAGAGGTAAGGCCAG 56
Db      20 CTCAGAGGTAAGGCCAG 2

RESULT 115
US-10-310-914A-971008/c
; Sequence 971008, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
```

```
; SEQ ID NO 971008
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-971008

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      40 GAGAGGTAAGGCCAGCG 58
Db      20 GAGAGGTAAGGCCAGCG 2

RESULT 116
US-10-310-914A-1087873
; Sequence 1087873, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1087873
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1087873

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 68.4%; Pred. No. 1.3e+02;
Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      36 CTCGAGAGGTAAGGCC 54
Db      1 CUCGAGAGGTAAGGAC 19

RESULT 117
US-10-310-914A-1313685/c
; Sequence 1313685, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1313685
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1313685

Query Match      18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGTAAGAG 52
Db      20 TTCTGTGAGAGGTAAGAG 2
```

```
RESULT 118
US-10-310-914A-1088471
; Sequence 1088471, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1088471
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1088471

Query Match      18.2%; Score 14; DB 1; Length 18;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTGAG 42
      :|||:|:|:|:|:|
Db 2 UGCAGUCCUCUGAG 15

RESULT 119
US-10-310-914A-1123448/c
; Sequence 1123448, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1123448
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1123448

Query Match      18.2%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 CTCTGGAGTCCTCT 39
      |||||:|:|:|:|
Db 19 CTCTGGAGTCCTCT 6

RESULT 120
US-11-101-244-686616
; Sequence 686616, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
```

```
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 686616
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-686616

Query Match      18.2%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 AAAGAGCCGCGAA 60
      |||||:|:|:|:|
Db 3 AAAGAGCCGCGAA 16

RESULT 121
US-11-083-784-686616
; Sequence 686616, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 686616
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-686616

Query Match      18.2%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 AAAGAGCCGCGAA 60
      |||||:|:|:|:|
Db 3 AAAGAGCCGCGAA 16

RESULT 122
US-10-310-914A-43662
; Sequence 43662, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
```



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; SEQ ID NO 43662
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-43

```

```
Query Match      18.2%; Score 14; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. NO. 1.3e+02;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
```

QY 64 GATGTCCTGTCAAG 77
||:|:|:|:|:|
Db 4 GAUGUCCUGUCAAG 17

RESULT 123
US-10-310-914A-732261
; Sequence 732261, Application US/10310914A
; Publication No. US20060003322A1

```

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 732261
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-732261

```

```
Query Match      17.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 1.6e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

Qy 50 GAGCCAGCGAAGCTGAT 66
|||||
Db 1 GAGCCAGCGCAGCUGCU 17

RESULT 124
US-10-310-914A-815753/c
; Sequence 815753, Application US/10310914A
; Publication No. US20060003322A1

```

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 815753
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-815753

```

```
Query Match      17.9%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.6e+02;
Matches 15: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 8 GACGGCCTGGGGTACA 24
| | | | | | | | | |
Db 17 GGCGGCCTGGGGGTACA 1

RESULT 125
US-10-310-914A-946707/c
; Sequence 946707, Application US/10310914A
; Publication No. US2006000332A1
; GENERAL INFORMATION:

```

? APPLICANT: BENICWACH, KESZAT
? APPLICANT: Shiler, Ivaaz
? TITLE OF INVENTION: Bioinformatically deter
? TITLE OF INVENTION: use thereof
? FILE REFERENCE: 06087-0200.CPUS01
? CURRENT APPLICATION NUMBER: US/10/310,914A
? CURRENT FILING DATE: 2002-12-06
? NUMBER OF SEQ ID NOS: 1388402
? SOFTWARE: Patent in version 3.3

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```

; SEQ ID NO 946707
;
; LENGTH: 18
;
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-946707

```

	Query Match	17.9%;
	Best Local Similarity	88.2%;
	Matches	15; Conservative
Qy	43	AGGTAAGAGCCAGCGA 5
Dh	18	AGGAGAGAGCCAGCGA 2

RESULT 126
US-10-310-914A-202536
; Sequence 202536, Application US/10310914A
; Publication No. US2006003322A1

```

? GENERAL INFORMATION:
? APPLICANT: Bentwich, Isaac
? APPLICANT: Shiler, Kvazat
? TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
? TITLE OF INVENTION: uses thereof
? FILE REFERENCE: 06087.0200.CPUS01
? CURRENT APPLICATION NUMBER: US/10/310,914A
? CURRENT FILING DATE: 2002-12-06
? NUMBER OF SEQ ID NOS: 1388402
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 202536
? LENGTH: 19
? TYPE: RNA
? ORGANISM: Human
US-10-310-914A-202536

```

Query Match	17.9%	Score 13.8	DB 1	Length 19
Best Local Similarity	82.4%	Pred. No. 1.5e+02		
Matches 14:	Conservative 1	Mismatches 2	Indels 0	Gaps 0

Qy 48 AAGAGCCAGCGAAGCTG 64
||| ||| ||| ||| :
Db 3 AAGAGACAGGGAAGCTG 19

RESULT 127
US-10-310-914A-760173/c
; Sequence 760173, Application US/10310914A
: Publication No. US2006003322A1

```

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087, 0200 CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 760173

```

```
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-760173

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACAGACGGCTGGG 18
Db 17 AAATAAGATGGCTGGG 1

RESULT 128
US-10-310-914A-785948
; Sequence 785948, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 785948
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-785948

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGCTGGGGATACAACT 27
Db 3 GGCCUGGGGACACAGCU 19

RESULT 129
US-10-310-914A-1194348
; Sequence 1194348, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1194348
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1194348

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 28 CTGGAGTCCTCTGAGAG 44
Db 2 CUUGUGUCCUCGACAG 18

RESULT 130
```

```
US-11-101-244-14272
; Sequence 14272, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 14272
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-14272

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTGTC 74
Db 2 GAAGUCGAGUCCUGUC 18

RESULT 131
US-11-101-244-67079
; Sequence 67079, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 67079
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-67079

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 28 CTGGAGTCCTCTGAGAG 44
Db 2 CUGGAGUCCUCGACAG 18

RESULT 132
US-11-101-244-98224/c
```

```
; Sequence 98224, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 98224
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-98224

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTGTC 74
DB 17 GAAGGTGATGTCCTGGC 1

RESULT 133
US-11-101-244-160889
; Sequence 160889, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 160889
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-160889

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCTGT 73
DB 1 CGAAGGGGAGUGUCCUGU 17

RESULT 134
US-11-101-244-160989
; Sequence 160989, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 160989
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-160989

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCTGT 73
DB 1 CGAAGGGGAGUGUCCUGU 17

RESULT 135
US-11-101-244-161088
; Sequence 161088, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-161088

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCTGT 73
DB 1 CGAAGGGGAGUGUCCUGU 17

RESULT 136
US-11-101-244-161190
; Sequence 161190, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-161190

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCTGT 73
DB 1 CGAAGGGGAGUGUCCUGU 17
```

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-161190

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGCTCTGT 73
DB 1 CGAAGGGGAGUGCCUGU 17

RESULT 137
US-11-101-244-197189
; Sequence 197189, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 197189
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-197189

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 52 GCCAGCGAGCTGATGT 68
DB 2 GCCAGAGUGAGUGU 18

RESULT 138
US-11-101-244-219953
; Sequence 219953, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 219953
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-219953

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 16 GGGGATACAACTCTGGA 32
DB 2 GAGGAUACAGCUCUGGA 18

RESULT 140
US-11-101-244-290226
; Sequence 290226, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

```

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 290226
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-290226

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCGCGAA 60
||:||||| ||| |||
Db 2 GGUAAGAGUCAGAGAA 18

RESULT 141
US-11-101-244-290240
; Sequence 290240, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 290240
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-290240

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCGCGAA 60
||:||||| ||| |||
Db 1 GGUAAGAGUCAGAGAA 17

RESULT 142
US-11-101-244-40405/c
; Sequence 40405, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 40405
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-40405

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37 TCTGAGAGGTAAAGAGC 53
||||| ||| ||| |||
Db 17 TCTGAGGATAAAGAGC 1

RESULT 143
US-11-101-244-440203
; Sequence 440203, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 440203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-440203

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACAAGAGCGCGCTGGG 18
||||| ||| ||| |||
Db 1 AAACAAGAGCGCGGUGG 17

RESULT 144
US-11-101-244-524859
; Sequence 524859, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 524859
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-524859

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 1.5e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      21  TACAACCTCTGGAGTCTCT 37
      :|||||:||||: :
Db      2  UAACAACUCUGGAUUGCU 18

RESULT 145
US-11-101-244-673690/c
; Sequence 673690, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 673690
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-673690

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14  CTGGGGATACAACCTCTG 30
      :|||||:|||||:
Db      18  CTGGGGGTACAACCTCTG 2

RESULT 146
US-11-101-244-681344
; Sequence 681344, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 681344
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-681344

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      59  AAGCTGATGTCCTGTCA 75
      :|||||:||||:
Db      1  AAGCUGAGGUCUGUGA 17

RESULT 148
US-11-101-244-731099/c
; Sequence 731099, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 727031
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-727031

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      23  CAACTCTGGAGTCTCTCT 39
      :|||||:||||:
Db      1  CAACACUGAGUCCUUAU 17

RESULT 147
US-11-101-244-727031
; Sequence 727031, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 727031
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-727031

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      23  CAACTCTGGAGTCTCTCT 39
      :|||||:||||:
Db      1  CAACACUGAGUCCUUAU 17
```

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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 731099
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-731099

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      24  AACTCTGGAGTCCTCTG 40
      ||||| ||||| |||||
Db      18  AACTCTGAATTCCTCTG 2

RESULT 149
US-11-101-244-731168/c
; Sequence 731168, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 731168
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-731168

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      24  AACTCTGGAGTCCTCTG 40
      ||||| ||||| |||||
Db      17  AACTCTGAATTCCTCTG 1

RESULT 150
US-11-101-244-751095/c
; Sequence 751095, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

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; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 751095
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-751095

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      35  CCTCTGAGAGGTAAAGA 51
      ||||| ||||| |||||
Db      18  CTCTGAGAGGTAAACA 2

RESULT 151
US-11-101-244-813171/c
; Sequence 813171, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 813171
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-813171

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      21  TACAACCTCTGGAGTCCT 37
      ||||| ||||| |||||
Db      19  TACAGCTCTGGAGTCCT 3

RESULT 152
US-11-101-244-862664/c
; Sequence 862664, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

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```
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 862664
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-862664

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 ACTCTGGAGTCTCTGGA 41
Db 17 ACACCGAGTCTCTGGA 1

RESULT 153
US-11-101-244-900906
; Sequence 900906, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 900906
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-900906

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAGAGCC 54
Db 2 CUGAGAGCUAAGAGAC 18

RESULT 154
US-11-101-244-941347/c
; Sequence 941347, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 941347
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-941347

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAGA 43
Db 19 TCTTGAGTCCACTGAGA 3

RESULT 155
US-11-101-244-959690
; Sequence 959690, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 959690
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-959690

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGCTCT 71
Db 2 AGUGAAGCUGAUGUUCU 18

RESULT 156
US-11-101-244-966428
; Sequence 966428, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 966428
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-966428

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAACAAGAGCGCCCTGG 17
Db 1 CAACAAGAGACCUAG 17

RESULT 157
US-11-101-244-1036369
; Sequence 1036369, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1036369
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1036369

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 45 GTAAAGAGCCAGCGAAG 61
Db 1 GCAAGAGCGACCGAAG 17

RESULT 158
US-11-101-244-1069062/c
; Sequence 1069062, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1069062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1069062

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 46 TAAAGAGCCAGCGAAGC 62
Db 19 TAAATGCCAGCGAAGC 3

RESULT 159
US-11-101-244-1149570
; Sequence 1149570, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1149570
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1149570

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 60 AGCTGATGTCCTGTCAA 76
Db 2 AGAUGAUGUCCUGGCAA 18

RESULT 160
US-11-101-244-1271626
; Sequence 1271626, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
```

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; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1271626
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1271626

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.2%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTGTC 74
Db 2 GAGGCAGAUCCUGUC 18

RESULT 161
US-11-101-244-1286508/c
; Sequence 1286508, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286508
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1286508

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTGTC 74
Db 18 GAAGATGAAGTCTCTGTC 2

RESULT 162
US-11-101-244-1286517/c
; Sequence 1286517, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286517
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1286517

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGCTCCT 71
Db 18 AGCAAGATGATGACCT 2

RESULT 163
US-11-101-244-1299503/c
; Sequence 1299503, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1299503
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1299503

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGCTCCT 71
Db 18 AGCAAGATGATGACCT 2

RESULT 164
US-11-101-244-1321159
; Sequence 1321159, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1321159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1321159

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGCTCCT 71
Db 18 AGCAAGATGATGACCT 2
```

```
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1321159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1321159

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGAGT 34
   ||:||||| |:|||||
Db 1 GGAUACACGACUGGAGU 17

RESULT 165
US-11-101-244-1334132
; Sequence 1334132, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1334132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1334132

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 35 CCTCTGAGAGGTAAGA 51
   ||:||||| |:|||||
Db 1 CCUCUGAGAGUCAAGA 17

RESULT 166
US-11-101-244-1359524
; Sequence 1359524, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359524
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1359524

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCGAA 60
   |:||||| |:|||||
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 167
US-11-101-244-1359621
; Sequence 1359621, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359621
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1359621

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCGAA 60
   |:||||| |:|||||
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 168
US-11-101-244-1453192/c
; Sequence 1453192, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1453192/c
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1453192/c

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCGAA 60
   |:||||| |:|||||
Db 1 GAUAAAGAGUCAGCGAA 17
```

```
; SOFTWARE: Proprietary
; SEQ ID NO 1453192
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1453192

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGTCCT 71
Db 18 AGAGAAGATGATGTCCT 2

RESULT 169
US-11-101-244-1510975
; Sequence 1510975, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1510975
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1510975

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 45 GTAAAGAGCCAGCGAAG 61
Db 1 GUGAAGAGCCAGUGAAG 17

RESULT 170
US-11-101-244-1565567/c
; Sequence 1565567, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

; SEQ ID NO 1565567
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1565567

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAGCT 63
Db 18 AATGAGCCAGCGAAGAT 2

RESULT 171
US-11-083-784-14272
; Sequence 14272, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 14272
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-14272

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTGTC 74
Db 2 GAAGUGAUGUCCUGUC 18

RESULT 172
US-11-083-784-67079
; Sequence 67079, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; SOFTWARE: Proprietary
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; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 67079
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-67079

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      28 CTGGAGTCCCTGAGAG 44
      |:|:|:|:|:|:|:|:|
Db      2 CUGGAGUCUCUGACAG 18

RESULT 173
US-11-083-784-98224/c
; Sequence 98224, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 98224
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-98224

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      58 GAAGCTGATGTCCTGTC 74
      |||||:|:|:|:|:|
Db      17 GAAGTGTATGTCCTGGC 1

RESULT 174
US-11-083-784-160889
; Sequence 160889, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 160889
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-160889

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      57 CGAAGCTGATGTCCTGT 73
      |||||:|:|:|:|:|
Db      1 CGAAGGGGAGUCCUGU 17

RESULT 175
US-11-083-784-160989
; Sequence 160989, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 160989
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-160989

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      57 CGAAGCTGATGTCCTGT 73
      |||||:|:|:|:|:|
Db      1 CGAAGGGGAGUCCUGU 17

RESULT 176
US-11-083-784-161088
; Sequence 161088, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-161088

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      57 CGAAGCTGATGTCCTGT 73
      |||||:|:~|:|:|:|
Db      1 CGAAGGGGAGUCCUGU 17

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; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161088
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-161088

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTCCTGT 73
      ||||| |||:|:|:|:|
Db 1 CGAAGGGGAGUGCCUGU 17

RESULT 177
US-11-083-784-161190
; Sequence 161190, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-161190

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTCCTGT 73
      ||||| |||:|:|:|:|
Db 1 CGAAGGGGAGUGCCUGU 17

RESULT 178
US-11-083-784-197189
; Sequence 197189, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 161190
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-197189

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTCCTGT 73
      ||||| |||:|:~|:|:|
Db 1 CGAAGGGGAGUGCCUGU 17

RESULT 179
US-11-083-784-219953
; Sequence 219953, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 219953
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-219953

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 37 TCTGAGAGGTAAAGAGC 53
      |:|:|:|:|:|:|:|
Db 1 UCUAAGAAGUAAGAGC 17

RESULT 180
US-11-083-784-276299
; Sequence 276299, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 219953
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-276299

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 37 TCTGAGAGGTAAAGAGC 53
      |:|:|:|:|:|:|:|
Db 1 UCUAAGAAGUAAGAGC 17

```

; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 276299
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-276299

Query Match 17.9%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 70.6%; Pred. No. 1.5e+02;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 16 GGGGATCAACTCTGGA 32
 |||||:|:|:|:|:|:|
 Db 2 GAGGAUACAGCUCUGGA 18

RESULT 181

US-11-083-784-290226
 ; Sequence 290226, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 290226
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-290226

Query Match 17.9%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCGAA 60
 ||:|||||:|:|:|:|:|
 Db 2 GGUAAGAGUCAGAGAA 18

RESULT 182

US-11-083-784-290240
 ; Sequence 290240, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 290240
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-290240

Query Match 17.9%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 82.4%; Pred. No. 1.5e+02;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCGAA 60
 ||:|||||:|:|:|:|:|
 Db 1 GGUAAGAGUCAGAGAA 17

RESULT 183

US-11-083-784-404405/c
 ; Sequence 404405, Application US/11083784
 ; Publication No. US20050245475A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmacon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 13499US
 ; CURRENT APPLICATION NUMBER: US/11/083,784
 ; CURRENT FILING DATE: 2005-03-18
 ; PRIOR FILING DATE: 2003-11-14
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 404405
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-083-784-404405

Query Match 17.9%; Score 13.8; DB 1; Length 19;
 Best Local Similarity 88.2%; Pred. No. 1.5e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 37 TCTGAGAGGTAAGAGC 53
 |||||:|:|:|:|:|:|
 Db 17 TCTGAGGATAAAGAGC 1

RESULT 184

US-11-083-784-440203

```
; Sequence 440203, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 440203
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-440203

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AAACAAGACGCGCTGGG 18
Db      1 AAACAAGACGCGCGUGG 17

RESULT 185
US-11-083-784-524859
; Sequence 524859, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 524859
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-524859

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 58.8%; Pred. No. 1.5e+02;
Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      21 TACAACCTCGAGTCCT 37
Db      2 UACAACUCUGGAGUUGCU 18

RESULT 186
US-11-083-784-673690/c
; Sequence 673690, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 673690
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-673690

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CTGGGATACACTCTG 30
Db      18 CTGAGGGTACACTCTG 2

RESULT 187
US-11-083-784-681344
; Sequence 681344, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 681344
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-681344

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      23 CAACTCTGGAGTCCTCT 39
```


Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 35 CCTCTGAGAGGTAAGA 51
| | | | | | | | | | | | | | | | | | | | | |
Db 18 CTCTGAGAGGTAACA 2

RESULT 192

US-11-083-784-813171/c
; Sequence 813171, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 813171
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-813171

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 21 TACACTCTGAGTCCT 37
| | | | | | | | | | | | | | | | | | | | | |
Db 19 TACAGCTCTGAGTTCT 3

RESULT 193

US-11-083-784-862664/c
; Sequence 862664, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 862664
; LENGTH: 19

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-862664

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 ACTCTGAGTCCTCTGA 41
| | | | | | | | | | | | | | | | | | | | | |
Db 17 ACACCGAGTCCTCTGA 1

RESULT 194

US-11-083-784-900906
; Sequence 900906, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 900906
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-900906

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 76.5%; Pred. No. 1.5e+02;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAGAGCC 54
| | | | | | | | | | | | | | | | | | | | | |
Db 2 CUGAGAGCUAAGAGAC 18

RESULT 195

US-11-083-784-941347/c
; Sequence 941347, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911

```

; SOFTWARE: Proprietary
; SEQ ID NO 941347
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-941347

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  27 TCTGAGTCTCTCTGAGA 43
    ||| ||||| |||||
Db  19 TCTTGAGTCCACTGAGA 3

RESULT 196
US-11-083-784-959690
; Sequence 959690, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 959690
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-959690

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy  55 AGCGAAGCTGATGTCCT 71
    || ||||| |||||
Db  2 AGUGAAGCUGAUGUUCU 18

RESULT 197
US-11-083-784-966428
; Sequence 966428, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

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; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 966428
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-966428

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy  1 CAAACAGACGCGCTGG 17
    ||||| ||||| |||||
Db  1 CAAACAGAGACCGUG 17

RESULT 198
US-11-083-784-1036369
; Sequence 1036369, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1036369
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1036369

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  45 GTAAAGAGCCGCGAAG 61
    ||||| ||||| |||||
Db  1 GCAAGAGCGCGAAG 17

RESULT 199
US-11-083-784-1069062/c
; Sequence 1069062, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

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; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1069062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1069062

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      46 TAAAGAGCCGACGAGC 62
      ||||| ||||| |||||
Db      19 TAAATGCCACGCGAGC 3

RESULT 200
US-11-083-784-1149570
; Sequence 1149570, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1149570
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1149570

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      60 AGCTGATGTCCTGTCAA 76
      ||||| ||||| |||||
Db      2 AGAUGAUGUCCUGGCAA 18

RESULT 201
US-11-083-784-1271626
; Sequence 1271626, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1271626
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1271626

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      58 GAAGCTGATGTCCTGTC 74
      ||||| ||||| |||||
Db      2 GAGGCAGAUCCUGUC 18

RESULT 202
US-11-083-784-1286508/c
; Sequence 1286508, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286508
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1286508

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      58 GAAGCTGATGTCCTGTC 74
      ||||| ||||| |||||
Db      18 GAAGATGAAGTCCTGTC 2

RESULT 203
US-11-083-784-1286517/c
; Sequence 1286517, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1271626
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1271626

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      46 TAAAGAGCCGACGAGC 62
      ||||| ||||| |||||
Db      19 TAAATGCCACGCGAGC 3

RESULT 200
US-11-083-784-1149570
; Sequence 1149570, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1149570
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1149570

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 64.7%; Pred. No. 1.5e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      60 AGCTGATGTCCTGTCAA 76
      ||||| ||||| |||||
Db      2 AGAUGAUGUCCUGGCAA 18

RESULT 201
US-11-083-784-1271626
; Sequence 1271626, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1286517
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1286517

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTGTC 74
    ||||| ||||| ||||| |||||
Db 19 GAAGATGAAGTCTGTC 3

RESULT 204
US-11-083-784-1299503/c
; Sequence 1299503, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1299503
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1299503

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGTCCT 71
    ||||| ||||| ||||| |||||
Db 18 AGCAAGAGCTGATGACCT 2

RESULT 205
US-11-083-784-1321159
; Sequence 1321159, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

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; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1321159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1321159

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 18 GGATACAACTCTCGAGT 34
    ||||| ||||| |||||
Db 1 GGAUACAGCACUGGAGU 17

RESULT 206
US-11-083-784-1334132
; Sequence 1334132, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1334132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1334132

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 70.6%; Pred. No. 1.5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 35 CCTCTGAGAGGTAAGA 51
    ||||| ||||| ||||| |||||
Db 1 CCUCUGAGAGUCACAGA 17

RESULT 207
US-11-083-784-1359524
; Sequence 1359524, Application US/11083784
; Publication No. US20050245475A1

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; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359524
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359524

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCAGCGAA 60
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 208
US-11-083-784-1359621
; Sequence 1359621, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359621
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359621

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCAGCGAA 60
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 209
US-11-083-784-1359621
; Sequence 1359621, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359621
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359621

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCAGCGAA 60
Db 1 GAUAAAGAGUCAGCGAA 17

RESULT 209
US-11-083-784-1359621
; Sequence 1359621, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1591911
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1510975

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 45 GTTAAAGAGCCAGCGAAG 61
Db 1 GUGAAGAGCCAGTGAAG 17

RESULT 210
US-11-083-784-1510975
; Sequence 1510975, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1510975
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1510975

Query Match 17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 45 GTTAAAGAGCCAGCGAAG 61
Db 1 GUGAAGAGCCAGTGAAG 17
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RESULT 211
US-11-083-784-1565567/c
; Sequence 1565567, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083.784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: US/10/714.333
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1565567
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1565567

Query Match      17.9%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      47 AAAGAGCCAGCGAGACT 63
Db      18 AATGAGCCAGCGAGAT 2

RESULT 212
US-10-310-914A-730939
; Sequence 730939, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 730939
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-730939

Query Match      17.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 1.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 ACAAGACGGCGCTGGG 18
Db      3 ACAAGACGGCGCUGUG 17

RESULT 213
US-10-310-914A-819956
; Sequence 819956, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 819956
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-819956

Query Match      17.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 1.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 ACAAGACGGCGCTGGG 18
Db      3 ACAAGACGGCGCUGUG 17

RESULT 214
US-10-310-914A-1127926
; Sequence 1127926, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1127926
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1127926

Query Match      17.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 73.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      31 GAGTCCTCTCAGAGG 45
Db      1 GAGGCTCUCAGAGG 15

RESULT 215
US-10-310-914A-715225
; Sequence 715225, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 715225
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-715225

Query Match      17.4%; Score 13.4; DB 1; Length 18;
Best Local Similarity 86.7%; Pred. No. 1.7e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 ACAAGACGGCGCTGGG 18
Db      3 ACAAGACGGCGCUGUG 17
```

```
Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAACAAGACGGCGCTG 16
   |||||
Db 1 AAACAAGACGGCGUUG 15
   |||||

RESULT 216
US-10-310-914A-751334
; Sequence 751334, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 751334
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-751334

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 22 ACAACTCTGGAGTCC 36
   ||| | | | | | |
Db 5 ACACCCUGGAGGUCC 19
   ||| | | | | | |

RESULT 217
US-10-310-914A-1053707
; Sequence 1053707, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1053707
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053707

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 42 GAGCTAAAGCGCCAG 56
   |||||
Db 3 GAGGUAACAGCCAG 17
   |||||

RESULT 218
US-10-310-914A-1058236
; Sequence 1058236, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1058236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1058236
```

```
Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 31 GAGTCCTCTGAGAGG 45
   ||| | | | | | |
Db 3 GAGUCCUCAGAGAGG 17
   ||| | | | | | |
```

```
RESULT 219
US-10-310-914A-1241072
; Sequence 1241072, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1241072
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1241072
```

```
Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAACAAGACGGCGCT 15
   |||||
Db 4 CAAACAACACGGCCU 18
   |||||
```

```
RESULT 220
US-10-310-914A-1268592/c
; Sequence 1268592, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1268592
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1268592
```



```
Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 44 GGTAAAGAGCCAGCG 58
Db 18 GGTAAAGAGAGCAGCG 4

RESULT 221
US-10-310-914A-1370512/c
; Sequence 1370512, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kruzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; PRIOR FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1370512
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1370512

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 22 ACAACTCTGGAGTCC 36
Db 17 AAAACTCTGGAGTCC 3

RESULT 222
US-11-101-244-24060/c
; Sequence 24060, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 24060
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-24060

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAAGAGC 53
Db 15 TGAGAGGCAAGAGC 1

RESULT 223
US-11-101-244-24159/c
; Sequence 24159, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 24159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-24159

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAAGAGC 53
Db 15 TGAGAGGCAAGAGC 1

RESULT 224
US-11-101-244-34612/c
; Sequence 34612, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 34612
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-34612

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 54 CAGCGAAGCTGATGT 68
Db 16 CAGTGAAGCTGATGT 2
```

RESULT 225

US-11-101-244-88668
; Sequence 88668, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 88668
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-88668

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGTCCT 71
|||||:|:|:|:
Db 4 CGAAGCUUAGUCU 18

RESULT 226

US-11-101-244-199690
; Sequence 199690, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 199690
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-199690

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAACAGACGGCCT 15
|||||:|:|:|:
Db 1 CAAACAGACGACCU 15

RESULT 227

US-11-101-244-387184

US-11-101-244-219414
; Sequence 219414, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 219414
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-219414

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAACAAGACGGCCT 15
|||||:|:|:|:
Db 1 CAAACAAGACGGCCU 15

RESULT 228

US-11-101-244-276236
; Sequence 276236, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 276236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-276236

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGATCAACTCTGGA 32
|||||:|:|:|:
Db 1 GGAUACAGCUCUGGA 15

; Sequence 387184, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387184
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-387184

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 46 TAAAGAGCCGCGAA 60
Db :||||||| |||||
2 UAAAGAGCCGCGAA 16

RESULT 230
US-11-101-244-387289
; Sequence 387289, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387289
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-387289

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 46 TAAAGAGCCGCGAA 60
Db :||||||| |||||
2 UAAAGAGCCGCGAA 16

RESULT 231
US-11-101-244-387392
; Sequence 387392, Application US/11101244

; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387392
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-387392

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 46 TAAAGAGCCGCGAA 60
Db :||||||| |||||
2 UAAAGAGCCGCGAA 16

RESULT 232
US-11-101-244-387492
; Sequence 387492, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387492
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-387492

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 46 TAAAGAGCCGCGAA 60
Db :||||||| |||||
2 UAAAGAGCCGCGAA 16

RESULT 233
US-11-101-244-410730/C
; Sequence 410730, Application US/11101244
; Publication No. US20050246794A1

```

; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349SUS
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 410730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-410730

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```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 31 GAGTCCTCTGAGAGG 45
Db 18 GAGTCCTCTGAGATG 4

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RESULT 234
US-11-101-244-410929/c
; Sequence 410929, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349SUS
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 410929
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-410929

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 31 GAGTCCTCTGAGAGG 45
Db 18 GAGTCCTCTGAGATG 4

```

```

RESULT 235
US-11-101-244-411027/c
; Sequence 411027, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349SUS
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 411027
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-411027

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 31 GAGTCCTCTGAGAGG 45
Db 18 GAGTCCTCTGAGATG 4

```

```

RESULT 236
US-11-101-244-512370/c
; Sequence 512370, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 1349SUS
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 512370
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-512370

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 22 ACAACTCTGAGGTCC 36
Db 15 ACAACACTGGAGTCC 1

```

```

RESULT 237
US-11-101-244-527876/c
; Sequence 527876, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.

```

; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 1349US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 527876
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-527876

Query Match 17.4%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 93.3%; Pred. No. 1.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCTGT 73
 |||||||||
 Db 19 AATCTGATGTCCTGT 5

RESULT 238
 US-11-101-244-539325
 ; Sequence 539325, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmoon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 1349US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 539325
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-539325

Query Match 17.4%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 60.0%; Pred. No. 1.6e+02;
 Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 63 TGATGTCCTGTCAAG 77
 :|||:|
 Db 3 UCAUGUCCUGUCAAG 17

RESULT 239
 US-11-101-244-550822
 ; Sequence 550822, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmoon, Inc.
 ; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 1349US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 550822
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-550822

Query Match 17.4%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 73.3%; Pred. No. 1.6e+02;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 30 GGAGTCTCTGAGAG 44
 |||||:|
 Db 1 GGAGUCCUCUGGAG 15

RESULT 240
 US-11-101-244-550923
 ; Sequence 550923, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmoon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela
 ; APPLICANT: Leake, Devin
 ; APPLICANT: Marshall, William
 ; APPLICANT: Scaringe, Stephen
 ; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
 ; FILE REFERENCE: 1349US
 ; CURRENT APPLICATION NUMBER: US/11/101,244
 ; CURRENT FILING DATE: 2005-04-07
 ; PRIOR APPLICATION NUMBER: 60/502,050
 ; PRIOR FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: 60/426,137
 ; PRIOR FILING DATE: 2002-11-14
 ; NUMBER OF SEQ ID NOS: 1591911
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 550923
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-101-244-550923

Query Match 17.4%; Score 13.4; DB 1; Length 19;
 Best Local Similarity 73.3%; Pred. No. 1.6e+02;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 30 GGAGTCTCTGAGAG 44
 |||||:|
 Db 1 GGAGUCCUCUGGAG 15

RESULT 241
 US-11-101-244-581627
 ; Sequence 581627, Application US/11101244
 ; Publication No. US20050246794A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dharmoon, Inc.
 ; APPLICANT: Khvorova, Anastasia
 ; APPLICANT: Reynolds, Angela

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 581627
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-581627
```

```
Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 37 TCTGAGAGTAAAGA 51
   |:|||||:|
Db 1 UCUCAGAGGUAAGA 15
```

```
RESULT 242
US-11-101-244-624448
; Sequence 624448, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmason, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 624448
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-624448
```

```
Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 58 GAAGCTGATGCTCTG 72
   |||||:|:|
Db 5 GAAGCUGAUGUCAUG 19
```

```
RESULT 243
US-11-101-244-680973
; Sequence 680973, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmason, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```

```
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 680973
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-680973
```

```
Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 59 AGCTGATGCTCTGT 73
   |||:|:|:|
Db 3 AGGCUGAUGCCUGU 17
```

```
RESULT 244
US-11-101-244-686033
; Sequence 686033, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmason, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 686033
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-686033
```

```
Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 18 GGATACAACTCTGGA 32
   |||:|:|:|
Db 1 GGAUACAACACUGGA 15
```

```
RESULT 245
US-11-101-244-710507
; Sequence 710507, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmason, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

```

; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 710507
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-710507

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCGAGGAG 61
   |||||
Db 3 AAAGAGCCGAGGAG 17

```

```

RESULT 246
US-11-101-244-710553
; Sequence 710553, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 710553
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-710553

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCGAGGAG 61
   |||||
Db 5 AAAGAGCCGAGGAG 19

```

```

RESULT 247
US-11-101-244-785114
; Sequence 785114, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785114
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-785114

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGAGGAA 60
   :|||||
Db 1 UAAAGAGCCGAGGAA 15

```

```

RESULT 248
US-11-101-244-785140
; Sequence 785140, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785140
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-785140

```

```

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGAGGAA 60
   :|||||
Db 2 UAAAGAGCCGAGGAA 16

```

```

RESULT 249
US-11-101-244-795267
; Sequence 795267, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

```

```
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 795267
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-795267
```

```
Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 63 TGATGTCCTGCTCAAG 77
Db 5 UGAUCCUGGUGCAAG 19
```

```
RESULT 250
US-11-101-244-833429
; Sequence 833429, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 833429
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-833429
```

```
Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 57 CGAAGCTGATGCTCT 71
Db 4 CAAAGCUGGUGCCU 18
```

```
RESULT 251
US-11-101-244-878459
; Sequence 878459, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
```

```
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 878459
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-878459
```

```
Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 60 AGCTGATGTCCTGTC 74
Db 2 AGCUGGUGCCUGUC 16
```

```
RESULT 252
US-11-101-244-972375/c
; Sequence 972375, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 972375
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-972375
```

```
Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 46 TAAAGAGCCAGCGAA 60
Db 19 TAAAGAGCCAGTGA 5
```

```
RESULT 253
US-11-101-244-972474/c
; Sequence 972474, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 972474
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-972474

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGCGAA 60
   |||||:|||||
Db 19 TAAAGAGCCAGTGAA 5

RESULT 254
US-11-101-244-1012488
; Sequence 1012488, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1012488
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1012488

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGTCGATGCTCTG 72
   ||||:|:|:|
Db 2 GAAGAUGAGUCCUG 16

RESULT 255
US-11-101-244-1034219/c
; Sequence 1034219, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
```

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; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1034219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1034219

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 60 AGCTGATGCTCTGTC 74
   |||||:|||||
Db 15 AGCTGATGCTCTGTC 1

RESULT 256
US-11-101-244-1036393
; Sequence 1036393, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1036393
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1036393

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCGCGAAG 61
   |||||:|||||
Db 2 AAAGAGCCGCGAAG 16

RESULT 257
US-11-101-244-1155168
; Sequence 1155168, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
```



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; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327400
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1327400

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTG 72
Db 18 GAAGCTGAGGTCCTG 4

RESULT 262
US-11-101-244-1327433/c
; Sequence 1327433, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327433
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1327433

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTG 72
Db 16 GAAGCTGAGGTCCTG 2

RESULT 263
US-11-101-244-1351972/c
; Sequence 1351972, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327433
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1351972

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTG 72
Db 16 GAAGCTGAGGTCCTG 2

RESULT 264
US-11-101-244-1359582
; Sequence 1359582, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359582
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1359582

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
Db 2 UAAAGAGUCAGCGAA 16

RESULT 265
US-11-101-244-1359676
; Sequence 1359676, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359676
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1359676

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
Db 2 UAAAGAGUCAGCGAA 16
```

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; SOFTWARE: Proprietary
; SEQ ID NO 1359676
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1359676

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGACGAA 60
Db 2 UAAAGAGCAGCGAA 16

RESULT 266
US-11-101-244-1418701
; Sequence 1418701, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1418701
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1418701

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 54 CAGCGAGCTGATGT 68
Db 1 CAGGAGCUGAUGU 15

RESULT 267
US-11-101-244-1435574/c
; Sequence 1435574, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1512594

; SEQ ID NO 1435574
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1435574

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGA 41
Db 15 TCTGGAGACCTCTGA 1

RESULT 268
US-11-101-244-1492356/c
; Sequence 1492356, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1492356
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-1492356

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGA 41
Db 17 TCTGGTGTCTCTGA 3

RESULT 269
US-11-101-244-1512594/c
; Sequence 1512594, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1512594
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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1512594

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGATACAACTCTGGA 32
Db 16 GGATACAACTCTGAA 2

RESULT 270
US-11-101-244-1522587
; Sequence 1522587, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1522587
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1522587

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 38 CTGAGAGGTAAGAG 52
Db 2 CUCAGAGGUAAGAG 16

RESULT 271
US-11-101-244-1560555
; Sequence 1560555, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1560555
; LENGTH: 19
; TYPE: RNA

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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1560555

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAACAAGACGGCCT 15
Db 1 CAAACAAGAUGGCCU 15

RESULT 272
US-11-101-244-1570062
; Sequence 1570062, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1570062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1570062

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGCGAAG 61
Db 2 AAAGAGCCAGGGAAG 16

RESULT 273
US-11-101-244-1570074
; Sequence 1570074, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1570074
; LENGTH: 19
; TYPE: RNA

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; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-24060

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAG 61
   |||||
Db 3 AAAGAGCCAGCGAAG 17

RESULT 274
US-11-083-784-24060/c
; Sequence 24060, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1590808
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-24060/c

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTG 72
   |||||
Db 2 GAAGCAGAUGUCCUG 16

RESULT 275
US-11-083-784-24060/c
; Sequence 24060, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 24060
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-24060/c

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAGAGC 53
   |||||
Db 15 TGAGAGGCAAGAGC 1

RESULT 276
US-11-083-784-24159/c
; Sequence 24159, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 24159
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-24159/c

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAGAGC 53
   |||||
Db 15 TGAGAGGCAAGAGC 1

RESULT 277
US-11-083-784-34612/c
; Sequence 34612, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 24060
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-24060/c

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTG 72
   |||||
Db 2 GAAGCAGAUGUCCUG 16
```



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; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 276236
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-276236

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGATACAACTCTCGA 32
Db 1 GGAUACAGCTCUGGA 15

RESULT 282
US-11-083-784-387184
; Sequence 387184, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387184
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387184

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGCGAA 60
Db 2 UAAAGAGCCGCGAA 16

RESULT 283
US-11-083-784-387289
; Sequence 387289, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387289
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387289

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGCGAA 60
Db 2 UAAAGAGCCGCGAA 16

RESULT 284
US-11-083-784-387392
; Sequence 387392, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387392
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387392

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGCGAA 60
Db 2 UAAAGAGCCGCGAA 16

RESULT 285
US-11-083-784-387492
; Sequence 387492, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 387492
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387492

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCGCGAA 60
Db 2 UAAAGAGCCGCGAA 16
```



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; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; SOFTWARE: Proprietary
; SEQ ID NO 387492
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-387492

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      46 TAAAGAGCCAGCGAA 60
Db      :|||||
        2 UAAAGAGCCUGCGAA 16

RESULT 286
US-11-083-784-410730/c
; Sequence 410730, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Marshall, William
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; SOFTWARE: Proprietary
; SEQ ID NO 410730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-410730

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      31 GAGTCCTCTGAGAGG 45
Db      :|||||
        18 GAGTCCTCTGAGATG 4

RESULT 287
US-11-083-784-410929/c
; Sequence 410929, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Marshall, William
; APPLICANT: Leake, Devin
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; SOFTWARE: Proprietary
; SEQ ID NO 410730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-410730

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      31 GAGTCCTCTGAGAGG 45
Db      :|||||
        18 GAGTCCTCTGAGATG 4

RESULT 288
US-11-083-784-411027/c
; Sequence 411027, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; SOFTWARE: Proprietary
; SEQ ID NO 411027
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-411027

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      31 GAGTCCTCTGAGAGG 45
Db      :|||||
        18 GAGTCCTCTGAGATG 4

RESULT 289
US-11-083-784-512370/c
; Sequence 512370, Application US/11083784
; Publication No. US20050245475A1
; APPLICANT: Khvorova, Anastasia
```

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; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 512370
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-512370

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 ACAACTCTGGAGTCC 36
Db 15 ACAACACTGGAGTCC 1

RESULT 290
US-11-083-784-527876/c
; Sequence 527876, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527876
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-527876

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AACCTGATCTCTGT 73
Db 19 AATCTGATCTCTGT 5

RESULT 291
US-11-083-784-527876/c
; Sequence 527876, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 527876
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-527876

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AACCTGATCTCTGT 73
Db 19 AATCTGATCTCTGT 5

RESULT 292
US-11-083-784-550822
; Sequence 550822, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 550822
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-550822

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 30 GGAGTCCTCTGAGAG 44
Db 1 GGAGUCCUCUGGAG 15
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; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-785114

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
   :|||||
Db 1 UAAAGAGCCGCGAA 15

RESULT 301
US-11-083-784-785140
; Sequence 785140, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785140
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-785140

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
   :|||||
Db 2 UAAAGAGCCGCGAA 16

RESULT 302
US-11-083-784-795267
; Sequence 795267, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 785140
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-785140

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 46 TAAAGAGCCGCGAA 60
   :|||||
Db 2 UAAAGAGCCGCGAA 16

RESULT 303
US-11-083-784-833429
; Sequence 833429, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 833429
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-833429

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGCTCT 71
   :|||||
Db 4 CAAAGCUGAUGUCCU 18

RESULT 304
US-11-083-784-878459
; Sequence 878459, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 833429
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-833429

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGCTCT 71
   :|||||
Db 4 CAAAGCUGAUGUCCU 18
```



```
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional sirna
; FILE REFERENCE: 13499US
; CURRENT FILING DATE: 2005-03-18
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1249609
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1249609

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTG 72
Db 15 GAAGCTGTTGTCCTG 1

RESULT 313
US-11-083-784-1326829/c
; Sequence 1326829, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional sirna
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1326829
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1326829

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 26 CTCGAGGATCCTCTG 40
Db 18 CTCGAGGCGCTCTG 4

RESULT 314
US-11-083-784-1327400/c
; Sequence 1327400, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional sirna
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327400
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1327400

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTG 72
Db 16 GAAGCTGAGGTCCTG 2

RESULT 315
US-11-083-784-1327433/c
; Sequence 1327433, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional sirna
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1327433
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1327433

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATGTCCTG 72
Db 16 GAAGCTGAGGTCCTG 2
```



```

RESULT 316
US-11-083-784-1351972/c
; Sequence 1351972, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1351972
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1351972

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      18 GGATACAACTCTGGA 32
      ||| ||||| ||||| |||||
DB      17 GGAGACAACTCTGGA 3

RESULT 317
US-11-083-784-1359582
; Sequence 1359582, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359582
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359582

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      46 TAAAGAGCGGCGAA 60
      :||||| ||||| |||||
DB      2 UAAAGAGCGGCGAA 16

RESULT 318
US-11-083-784-1359676
; Sequence 1359676, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1359676
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1359676

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      46 TAAAGAGCGGCGAA 60
      :||||| ||||| |||||
DB      2 UAAAGAGCGGCGAA 16

RESULT 319
US-11-083-784-1418701
; Sequence 1418701, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1418701
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1418701

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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```
QY 54 CAGCGAAGCTGTGT 68
    ||| |||||:|:|:|
Db 1 CAGUGAAGCUGAUGU 15

RESULT 320
US-11-083-784-1435574/c
; Sequence 1435574, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1435574
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1435574

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGA 41
    ||||| |||||
Db 15 TCTGGAGACCTCTGA 1

RESULT 321
US-11-083-784-1492356/c
; Sequence 1492356, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1492356
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1492356

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGA 41
    ||||| |||||
Db 15 TCTGGAGACCTCTGA 1

RESULT 322
US-11-083-784-1512594/c
; Sequence 1512594, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1512594
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1512594

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGA 32
    ||||| |||||
Db 16 GGATACAACTCTGAA 2

RESULT 323
US-11-083-784-1522587
; Sequence 1522587, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1522587
; LENGTH: 19
; TYPE: RNA
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; ORGANISM: Homo sapiens
US-11-083-784-1522587

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 38 CTGAGAGGTTAAGAG 52
   |:|||||:|||||
Db 2 CUCAGAGGUAAGAG 16

RESULT 324
US-11-083-784-1560555
; Sequence 1560555, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1560555
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1560555

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 1.6e+02;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAACAGAGCGGCT 15
   |||||||:|||||
Db 1 CAAACAGAGGCGCU 15

RESULT 325
US-11-083-784-1570062
; Sequence 1570062, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
US-11-083-784-1570062

; SEQ ID NO 1570062
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1570062

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCGCGAAG 61
   |||||||:|||||
Db 2 AAAGAGCCGCGAAG 16

RESULT 326
US-11-083-784-1570074
; Sequence 1570074, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1570074
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1570074

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCGCGAAG 61
   |||||||:|||||
Db 3 AAAGAGCCGCGAAG 17

RESULT 327
US-11-083-784-1590808
; Sequence 1590808, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
US-11-083-784-1590808

; SEQ ID NO 1590808
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1590808

Query Match      17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCGCGAAG 61
   |||||||:|||||
Db 3 AAAGAGCCGCGAAG 17
```

; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1590808
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1590808

Query Match 17.4%; Score 13.4; DB 1; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.6e+02;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 58 GAAGCTGATCTCTG 72
||||| |||:|:|:
Db 2 GAAGCAGAUCCUG 16

RESULT 328
US-10-310-914A-128513/c
; Sequence 128513, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128513
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-128513

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 40 GAGAGGTAAAGCCAGC 57
||||| | |||||
Db 18 GAGAGGGAGAGCGAGC 1

RESULT 329
US-10-310-914A-176877
; Sequence 176877, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 176877
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-176877

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.8e+02;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 35 CCTCTGAGAGTAAAGAG 52
||:|:||||| |||||

Db 1 CCUCUGAGAGUGAAGGAG 18

RESULT 330
US-10-310-914A-721777
; Sequence 721777, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 721777
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-721777

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGCCAGCG 58
||||| ||||| |||||
Db 1 AGAGGAAAGAGAAAGCG 18

RESULT 331
US-10-310-914A-794232
; Sequence 794232, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 794232
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-794232

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 28 CTGGAGTCCTCTGAGAGG 45
|||:|:|:|:|:|:|
Db 1 CAGGAGUCCUCUAGGAGG 18

RESULT 332
US-10-310-914A-956449
; Sequence 956449, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06

; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 956449
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-956449

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAACAAGACGCGCTGGGG 19
DB 1 AGACAGGAGGCCUGGG 18

RESULT 333

US-10-310-914A-970022/c
; Sequence 970022, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 970022
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-970022

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 38 CTGAGAGGTAAGAGCCA 55
DB 18 CTGAGAGCTTAAGAGCTA 1

RESULT 334

US-10-310-914A-1268240/c
; Sequence 1268240, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1268240
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1268240

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 25 ACTCTGAGTCCTCTGAG 42
DB 18 ACTCTGAATCCTATGG 1

RESULT 335

US-10-310-914A-1213531
; Sequence 1213531, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1213531
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1213531

Query Match 16.9%; Score 13; DB 1; Length 18;
Best Local Similarity 69.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 26 CTCCTGAGTCCTC 38
DB 6 CUCUGGAGUCCUC 18

RESULT 336

US-10-750-185-15896/c
; Sequence 15896, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15896
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-750-185-15896

Query Match 16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 42 GAGGTAAAGAGCCAGC 57
DB 16 GAGGTTAGGAGCCAGC 1

RESULT 337

US-10-750-623-15896/c
; Sequence 15896, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:

```
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15896
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer
US-10-750-623-15896

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;

QY 42 GAGGTAAGGCCAGC 57
Db 16 GAGGTTAGGCCAGC 1
      ||||| ||||| |||||

RESULT 338
US-10-310-914A-198185
; Sequence 198185, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 198185
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-198185

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 2;

QY 12 GCCTGGGGATACAACT 27
Db 3 GCCAGGGAUAACAACU 18
      ||| ||||| |||||

RESULT 339
US-10-310-914A-319191
; Sequence 319191, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
```

```
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 319191
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-319191

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 75.0%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 2;

QY 37 TCTGAGAGGCTAAAGAG 52
Db 3 UCUGAGAGGCACAGAG 18
      :||| ||||| |||||

RESULT 340
US-10-310-914A-537246/c
; Sequence 537246, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 537246
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-537246

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 59 AAGCTGATGTCCTGTC 74
Db 17 AAGCTGATTCCTGCC 2
      ||||| ||||| |||||

RESULT 341
US-10-310-914A-560230/c
; Sequence 560230, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 560230
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-560230

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;

QY 29 TGGAGTCCTCTGAGAG 44
Db 16 TGGAGGCTCTGGGAG 1
      ||||| ||||| |||||
```

```
RESULT 342
US-10-310-914A-575025
; Sequence 575025, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 575025
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-575025

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      34  TCCTCTGAGAGGTAAA 49
      :||:|: ||| |:|||
Db      1  UCCUCUAGAAGUAA 16

RESULT 343
US-10-310-914A-586396/c
; Sequence 586396, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 586396
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-586396

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      34  TCCTCTGAGAGGTAAA 49
      :||:|: ||| |:|||
Db      1  UCCUCUAGAAGUAA 16

RESULT 344
US-10-310-914A-784421
; Sequence 784421, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 784421
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-784421

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      49  AGAGCCAGCGAAGCTG 64
      ||||| ||||| |||||
Db      3  AGAGGGAGCGAAGCUG 18

RESULT 345
US-10-310-914A-815477
; Sequence 815477, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 815477
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-815477

Query Match      16.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      35  CCTCTGAGAGGTAAAG 50
      ||:| ||||| |||||
Db      3  CCUCAGAGGCGAAG 18

RESULT 346
US-10-310-914A-919520/c
; Sequence 919520, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 919520
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-919520

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      50  GAGCCAGCGAAGCTGA 65
      ||||| ||||| |||||
Db      17  GAGCCGCGAAGCGGA 2

RESULT 347
US-10-310-914A-919520
; Sequence 919520, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 919520
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-919520

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      43  AGGTAAAGAGCCAGCG 58
      ||||| ||||| |||||
Db      18  AGGTGAAGAGCCAGCG 3
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 784421
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-784421

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      49  AGAGCCAGCGAAGCTG 64
      ||||| ||||| |||||
Db      3  AGAGGGAGCGAAGCUG 18

RESULT 345
US-10-310-914A-815477
; Sequence 815477, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 815477
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-815477

Query Match      16.8%; Score 12.8; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      35  CCTCTGAGAGGTAAAG 50
      ||:| ||||| |||||
Db      3  CCUCAGAGGCGAAG 18

RESULT 346
US-10-310-914A-919520/c
; Sequence 919520, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 919520
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-919520

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      43  AGGTAAAGAGCCAGCG 58
      ||||| ||||| |||||
Db      18  AGGTGAAGAGCCAGCG 3
```

```
RESULT 347
US-10-310-914A-1087593
; Sequence 1087593, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1087593
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1087593

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 15 TGGGGATACAACTCTG 30
Db 1 UGGGGCUACACCUUG 16

RESULT 348
US-10-310-914A-1209729/c
; Sequence 1209729, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1209729
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1209729

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 61 GCTGATGTCCTGTGCAA 76
Db 16 GCTGATGTCCTGACCA 1

RESULT 349
US-10-310-914A-1353151
; Sequence 1353151, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
```

```
; SEQ ID NO 1353151
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1353151

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 81.2%; Pred. No. 2e+02;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCTGA 65
Db 2 GAGACAGCGAAGCTCA 17

RESULT 350
US-10-310-914A-1354913
; Sequence 1354913, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1354913
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1354913

Query Match      16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 AAAGAGCCGCGAAGC 62
Db 3 AAAGAGACAGAGAAGC 18

RESULT 351
US-10-505-263-37/c
; Sequence 37, Application US/10505263
; Publication No. US20060014940A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Case Western Reserve University
; APPLICANT: The Brigham and Women's Hospital, Inc.
; APPLICANT: Mount, David B
; APPLICANT: Romero, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF SLC26A6, SLC26A1, and SLC26A2
; FILE REFERENCE: 1242/50/2 PCT/US
; CURRENT APPLICATION NUMBER: US/10/505,263
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US 60/360,275
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: PCT/US03/06469
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-505-263-37

Query Match      15.6%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
```


Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GACGGCCTGGGG 19

Db 12 GACGGCCTGGGG 1

Search completed: April 19, 2006, 16:15:44
Job time : 1 secs

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GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioacceleration Ltd.
 OW nucleic - nucleic search, using sw model
 Run on: April 19, 2006, 16:06:39 ; Search time 0.001 Seconds
 (without alignments)
 403.480 Million cell updates/sec

Title: US-10-643-038-17_994-1070
 Perfect score: 77
 Sequence: 1 caacaagaagcctg999a.....gaagctgatgtcctgtcaag 77

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 0.5
 Searched: 181 seqs, 2620 residues

Total number of hits satisfying chosen parameters: 362

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 182 summaries

Database : gedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	28.2	36.6	33	1 A23021	ACCESSION:A23021
C 2	28.2	36.6	33	1 I23840	ACCESSION:I23840
C 3	21	27.3	21	1 AR074251	ACCESSION:AR074251
C 4	21	27.3	21	1 AX032613	ACCESSION:AX032613
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C 6	14.8	19.2	20	1 BD089289	ACCESSION:BD089289
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C 19	13.4	17.4	17	1 AR466351	ACCESSION:AR466351
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C 22	13.4	17.4	17	1 AX674032	ACCESSION:AX674032
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C 24	13.4	17.4	17	1 AX738057	ACCESSION:AX738057
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C 26	13.2	17.1	18	1 AR166421	ACCESSION:AR166421
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C 75	10.8	14.0	15	1 AR113242	ACCESSION:AR113242
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C 77	10.8	14.0	15	1 CS004710	ACCESSION:CS004710
C 78	10.8	14.0	15	1 CS004712	ACCESSION:CS004712
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C 81	10.8	14.0	15	1 I39320	ACCESSION:I39320
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C 84	10.8	14.0	15	1 AX635599	ACCESSION:AX635599
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155 9.4 12.2 11 1 CS058436 ACCESSION:CS058436
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179 9.4 12.2 13 1 AR285769 ACCESSION:AR285769

180 9.4 12.2 13 1 AR397760 ACCESSION:AR397760
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182 9.4 12.2 13 1 AX813993 ACCESSION:AX813993

ALIGNMENTS

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DEFINITION 3' oligonucleotide.
ACCESSION A23021
VERSION A23021.1 GI:833241
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 33)
AUTHORS
TITLE EXPRESSION SYSTEMS
JOURNAL Patent: WO 92/1380-A 3 09-JUL-1992;
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/mol_type="unassigned DNA"
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LOCUS I23840 33 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 4 from patent US 553885.
ACCESSION I23840
VERSION I23840.1 GI:1603710
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Hollis,M., Needham,M.R.C., Gooding,C., Grosveld,F.G. and Antoniou,M.
TITLE Expression systems
JOURNAL Patent: US 553885-A 4 23-JUL-1996;
FEATURES Location/Qualifiers
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Query Match 36.6%; Score 28.2; DB 1; Length 33;
Best Local Similarity 90.9%; Pred. No. 0.1;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 33 GACGGCTGGGATACAACTCTGGAGTCTCTG 1

RESULT 3
AR074251/c
LOCUS AR074251 21 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 59 from patent US 5952490.
ACCESSION AR074251
VERSION AR074251.1 GI:10001006
KEYWORDS

SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y., Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and Imbach,J.Louis.
 TITLE Oligonucleotides having a conserved G4 core sequence
 JOURNAL Patent: US 5952490-A 59 14-SEP-1999;
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 Db 21 ATCAACTCTGGAGTCCTCTG 1
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 AX032613/c
 LOCUS AX032613 21 bp DNA linear PAT 20-SEP-2000
 DEFINITION Sequence 59 from Patent EP1016715.
 ACCESSION AX032613
 VERSION AX032613.1 GI:10279551
 KEYWORDS
 SOURCE unidentified
 ORGANISM unclassified sequences.
 REFERENCE 1
 AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J., Bennett,C.P., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and Wyatt,J.R.
 TITLE Oligonucleotides having a conserved G4 core sequence
 JOURNAL Patent: EP 1016715-A 59 05-JUL-2000;
 ISIS PHARMACEUTICALS INC (US)
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 Db 21 ATCAACTCTGGAGTCCTCTG 1
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 BD185713
 LOCUS BD185713 22 bp DNA linear PAT 17-JUN-2003
 DEFINITION Application of KIAA0172 gene functions for therapeutics, diagnosis , and pharmaceuticals.
 ACCESSION BD185713
 VERSION BD185713.1 GI:31877913
 KEYWORDS JP 2002369696-A/14.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Kiyama,R., Kitajima,K., Oguchi,S., Oishi,M., Ohara,O. and Nagase,T.
 TITLE Application of KIAA0172 gene functions for therapeutics, diagnosis, and pharmaceuticals
 JOURNAL Patent: JP 2002369696-A 14 24-DEC-2002;
 NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY, INFO GENES CO LTD, KAZUSA DNA RESEARCH INSTITUTE

COMMENT OS Artificial Sequence
 PN JP 2002369696-A/14
 PD 24-DEC-2002
 PF 01-APR-2002 JP 2002099422
 PI RYOICHI KIYAMA, KEISUKE KITAJIMA, SHINOBU OGUCHI, MICHIO OISHI, OSAMU OHARA,
 PI TAKAHIRO NAGASE
 PC C12N15/09,A61K31/711,A61K35/76,A61K38/00,A61K48/00,A61P35/00,
 PC C12Q1/68,
 G01N33/48,G01N33/48,G01N33/53,G01N33/566,G01N33/574,G01N33/574, PC
 C12N15/00,
 PC A61K37/02
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 /mol_type="genomic DNA"
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 Best Local Similarity 94.1%; Pred. No. 14;
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 Db 2 AGCTGATGCTGCTCAA 18
 RESULT 6
 BD089289/c
 LOCUS BD089289 20 bp DNA linear PAT 27-AUG-2002
 DEFINITION A method of arraying genome clone.
 ACCESSION BD089289
 VERSION BD089289.1 GI:22634899
 KEYWORDS JP 2001321190-A/1533.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Soeda,E.
 TITLE A method of arraying genome clone
 JOURNAL Patent: JP 2001321190-A 1533 20-NOV-2001;
 THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA GENOTECHS
 COMMENT OS Artificial Sequence
 PN JP 2001321190-A/1533
 PD 20-NOV-2001
 PF 12-MAR-2001 JP 2001068285
 PI EIICHI SOEDA
 PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
 C12N15/00,
 PC C12N15/00
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 Location/Qualifiers
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RESULT 12
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ACCESSION
  AR085604
VERSION
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KEYWORDS
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SOURCE
  Unknown.
ORGANISM
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REFERENCE
  1 (bases 1 to 18)
  Cowsett,D.M.
  TITLE
    Antisense modulation of G-alpha-13 expression
  JOURNAL
    Patent: US 5981732-A 40 09-NOV-1999;
  FEATURES
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Db 17 CCTGGGAGACAACCT 2

RESULT 13
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DEFINITION
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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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ORGANISM
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  Homiidae; Homo.
REFERENCE
  1
  Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
  Shannon,M.E.
  TITLE
    Myosin-like gene expressed in human heart and muscle
  JOURNAL
    Patent: WO 0192524-A 10024 06-DEC-2001;
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DEFINITION
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ACCESSION
  AR466348
VERSION
  AR466348.1 GI:42701405
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CQ625285
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DEFINITION
  Sequence 10025 from Patent WO0192524.
ACCESSION
  CQ625285
VERSION
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KEYWORDS
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SOURCE
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ORGANISM
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  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homiidae; Homo.
REFERENCE
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  Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
  Shannon,M.E.
  TITLE
    Myosin-like gene expressed in human heart and muscle
  JOURNAL
    Patent: WO 0192524-A 10025 06-DEC-2001;
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RESULT 15
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DEFINITION
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ACCESSION
  AR466347
VERSION
  AR466347.1 GI:42701404
KEYWORDS
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SOURCE
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ORGANISM
  Unclassified.
REFERENCE
  1 (bases 1 to 17)
  Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
  Shannon,M.E.
  TITLE
    Polynucleotide encoding a human myosin-like polypeptide expressed
    predominantly in heart and muscle
  JOURNAL
    Patent: US 6686188-A 10024 03-FEB-2004;
    Amersham PLC; Buckinghamshire;
  FEATURES
    source
      Location/Qualifiers
        1. .17
          /organism="unknown"
          /mol_type="genomic DNA"

Query Match
Best Local Similarity 18.2%; Score 14; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCTG 40
Db 4 TCTGGAGTCTCTCTG 17

RESULT 16
AR466348
LOCUS
DEFINITION
  Sequence 10025 from patent US 6686188.
ACCESSION
  AR466348
VERSION
  AR466348.1 GI:42701405
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KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 686188-A 10025 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;

FEATURES
source
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 18.2%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCG 40
|||||
Db 3 TCTGGAGTCTCTCG 16

RESULT 17
AX649090/c
LOCUS AX649090 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 930 from Patent EP1273660.
ACCESSION AX649090
VERSION AX649090.1 GI:29151908
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 930 08-JAN-2003; Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 17.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAGCT 63
|||||
Db 17 AATGAGCCAGCGAAGAT 1

RESULT 18
CQ625288
LOCUS CQ625288 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 10028 from Patent WO0192524.
ACCESSION CQ625288
VERSION CQ625288.1 GI:41675506
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10028 06-DEC-2001; Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGGAGTCTCTCTGAG 42
|||||
Db 1 CTGGAGTCTCTCTG 15

RESULT 19
AR466351
LOCUS AR466351 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 10028 from patent US 686188.
ACCESSION AR466351
VERSION AR466351.1 GI:42701408
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 686188-A 10028 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;

FEATURES
source
1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGGAGTCTCTCTGAG 42
|||||
Db 1 CTGGAGTCTCTCTG 15

RESULT 20
AX649091/c
LOCUS AX649091 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 931 from Patent EP1273660.
ACCESSION AX649091
VERSION AX649091.1 GI:29151909
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 931 08-JAN-2003; Aeomica, Inc. (US)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"


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Query Match      17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 47 AAAGAGCCAGCGAAG 61
Db 16 AATGAGCCAGCGAAG 2

RESULT 21	AX649092/c	AX649092	17 bp	DNA	linear	PAT 22-MAR-2003
LOCUS		Sequence 932 from Patent EP1273660.				
DEFINITION						

VERSION	AX649092.1	GI:29151910
KEYWORDS	.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Euarchontoglires; Primates; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Gu, Y.	
TITLE	Human sodium-hydrogen exchanger like protein 1	
JOURNAL	Patent: EP 1273660-A 932 08-JAN-2003; Amega, Inc. (US)	

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source
1. 17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 26;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 47 AAAGAGCCAGCGAG 61
Dp 15 AATGAGCCAGCGAG 1

RESULT 22	AX674032/c	AX674032	17 bp	DNA	linear	PAT 27-MAR-2003
LOCUS						
DEFINITION		Sequence 2477 from Patent WO03004526.				

AX674032	AX674032.1	GI:29332380
KEYWORDS		
SOURCE		
ORGANISM	Homo sapiens (human)	
	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Telerman, A., Anson, R. and Tufinder, M.	
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and their use as medicines	
JOURNAL	Patent: WO 03004526-A 2477 16-JAN-2003;	
	Molecular Engines Laboratories (FR)	
FEATURES	Location/Qualifiers	

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1: 2.7
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred.No. 26;
Matches 14; Conservative 1; Indels 0; Gaps 0;

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Qy 29 TGGAGTCTCTGAGA 43
Db 17 TGGAGTCTTCTGAGA 3

RESULT 23	AX732023/c	AX732023	Sequence 3657 from Patent WO03025175.	17 bp	DNA	linear	PAT 08-MAY-2003
LOCUS	AX732023	AX732023					
DEFINITION	AX732023	AX732023					
ACCESSION	AX732023.1	GI:30511366					
VERSION							

REFERENCE	1	Demant, A., Amson, R. and Tuijthof, M.
AUTHORS		
TITLE		Sequences involved in phenomena of tumour suppression, tumour
		reversion, apoptosis and/or virus resistance and their use as
		medicines
JOURNAL		Patent: WO 03025175-A 3657 27-MAR-2003 ;
FEATURES		Molecular Engines Laboratories (FR)
source		Location/Qualifiers
		1. .17
		/organism="Homo sapiens"
		/mol_type="unassigned DNA"
		/db_xref="taxon:9606"

Query Match	17.4%	Score 13.4; DB 1; Length 17;
Best Local Similarity	93.3%;	Pred. No. 26;
Matches 14; Conservative	0; Mismatches	1; Indels 0; Gaps 0;
Qy	29	TTGGAGTCCTCTGAGA 43
Db	17	TTGGAGTCCTCTGAGA 3

RESULT 24
AX738057/C

DEFINITION	Sequence 367, from faecal WO03023177.
ACCESSION	AX738057
VERSION	AX738057.1 GI:30517345
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE	1	Amann, C., Homol, J.
AUTHORS		Telerman, A., Amson, R. and Tuijnder, M.
TITLE		Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
JOURNAL		Patent: WO 03025177-A 3647 27-MAR-2003;
FEATURES		Molecular Engines Laboratories (FR)
source		Location/Qualifiers
		1. .17
		/organism="Homo sapiens"
		/mol_type="unassigned DNA"
		/db_xref="taxon:9606"

Query Match	17.4%	Score 13.4;	DB 1;	Length 17;
Best Local Similarity	93.3%;	Pred. No. 26;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps 0;				
Qy	29	GGAGTCTCTGAGA	43	
Db	17	GGAGTCTCTGAGA	3	

RESULT 25
AX762421/C

RESULT 25	PAR 25-JUN-2003
AX762421/c	
LOCUS	
AX762421	17 bp
	DNA
	linear

DEFINITION	Sequence 5742 from Patent WO03040369.
ACCESSION	AX762421
VERSION	AX762421.1 GI:32257037
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Teleman,A., Anson,R. and Tuijnder,M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines Patent: WO 03040369-A 5742 15-MAY-2003; Molecular Engines Laboratories (PR) Location/Qualifiers
AUTHORS	1..17
TITLE	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
JOURNAL	
FEATURES	source
Query Match	17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity	93.3%; Pred. No.26;
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	29 TGGAGTCCTCTGAGA 43
Db	17 TGGAGTCCTCTGAGA 3
RESULT 26	
AR166421/c	
LOCUS	AR166421 18 bp DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 14 from patent US 6280998.
ACCESSION	AR166421
VERSION	AR166421.1 GI:16241735
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
TITLE	Purified thermostable pyrococcus furiosus DNA ligase
JOURNAL	Patent: US 6280998-A 14 28-AUG-2001;
FEATURES	Location/Qualifiers
source	1..18 /organism="unknown" /mol_type="unassigned DNA"
Query Match	17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity	83.3%; Pred. No.29;
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	18 GGATACAACCTCTGGAGTC 35
Db	18 GGATACAACCTCTGGAGTC 1
RESULT 27	
AR166424	
LOCUS	AR166424 18 bp DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 17 from patent US 6280998.
ACCESSION	AR166424
VERSION	AR166424.1 GI:16241740
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
TITLE	Purified thermostable pyrococcus furiosus DNA ligase
JOURNAL	Patent: US 6280998-A 17 28-AUG-2001;
DEFINITION	Sequence 5742 from Patent WO03040369.
ACCESSION	AX762421
VERSION	AX762421.1 GI:32257037
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Teleman,A., Anson,R. and Tuijnder,M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines Patent: WO 03040369-A 5742 15-MAY-2003; Molecular Engines Laboratories (PR) Location/Qualifiers
AUTHORS	1..17
TITLE	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
JOURNAL	
FEATURES	source
Query Match	17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity	93.3%; Pred. No.26;
Matches	14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	29 TGGAGTCCTCTGAGA 43
Db	17 TGGAGTCCTCTGAGA 3
RESULT 26	
AR166421/c	
LOCUS	AR166421 18 bp DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 14 from patent US 6280998.
ACCESSION	AR166421
VERSION	AR166421.1 GI:16241735
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
TITLE	Purified thermostable pyrococcus furiosus DNA ligase
JOURNAL	Patent: US 6280998-A 14 28-AUG-2001;
FEATURES	Location/Qualifiers
source	1..18 /organism="unknown" /mol_type="unassigned DNA"
Query Match	17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity	83.3%; Pred. No.29;
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	18 GGATACAACCTCTGGAGTC 35
Db	18 GGATACAACCTCTGGAGTC 1
RESULT 27	
AR166424	
LOCUS	AR166424 18 bp DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 17 from patent US 6280998.
ACCESSION	AR166424
VERSION	AR166424.1 GI:16241740
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
TITLE	Purified thermostable pyrococcus furiosus DNA ligase
JOURNAL	Patent: US 6280998-A 17 28-AUG-2001;
DEFINITION	Sequence 5742 from Patent WO03040369.
ACCESSION	AX762421
VERSION	AX762421.1 GI:32257037
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Teleman,A., Anson,R. and Tuijnder,M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines Patent: WO 03040369-A 5742 15-MAY-2003; Molecular Engines Laboratories (PR) Location/Qualifiers
AUTHORS	1..17
TITLE	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
JOURNAL	
FEATURES	source
Query Match	17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity	83.3%; Pred. No.29;
Matches	15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	18 GGATACAACCTCTGGAGTC 35
Db	18 GGATACAACCTCTGGAGTC 1
RESULT 27	
AR166424	
LOCUS	AR166424 18 bp DNA linear PAT 17-OCT-2001
DEFINITION	Sequence 17 from patent US 6280998.
ACCESSION	AR166424
VERSION	AR166424.1 GI:16241740
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 18)
AUTHORS	Mathur,E.J., Marsh,E.J. and Schoettlin,W.E.
TITLE	Purified thermostable pyrococcus furiosus DNA ligase
JOURNAL	Patent: US 6280998-A 17 28-AUG-2001;
DEFINITION	Sequence 5742 from Patent WO03040369.
ACCESSION	AX762421
VERSION	AX762421.1 GI:32257037
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Teleman,A., Anson,R. and Tuijnder,M. Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines Patent: WO 03040369-A 5742 15-MAY-2003; Molecular Engines Laboratories (PR) Location/Qualifiers
AUTHORS	1..17
TITLE	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
JOURNAL	</

Query Match	17.1%;	Score 13.2;	DB 1;	Length 18;	
Best Local Similarity	83.3%;	Pred. No. 29;			
Matches	15;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;

Qy	30	GGAGTCCTCTGAGAGGTA	47		
Db	18	GGAGTCGTAGGAGGTA	1		

RESULT 33					
AX207952/c					
LOCUS	AX207952	18 bp	DNA	linear	PAT 31-AUG-2001
DEFINITION	Sequence 56 from Patent WO0157194.				
ACCESSION	AX207952				
VERSION	AX207952.1	GI:15422550			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1				
AUTHORS	Madison,E.L., Ong,E.O. and Yeh,J.C.				
TITLE	Nucleic acid molecules encoding transmembrane serine proteases, the				
	encoded proteins and methods based thereon				
JOURNAL	Patent: WO 0157194-A 56 09-AUG-2001;				
	CORVAS INTERNATIONAL, INC. (US)				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="Oligonucleotide Primer"				

Query Match	17.1%;	Score 13.2;	DB 1;	Length 18;	
Best Local Similarity	83.3%;	Pred. No. 29;			
Matches	15;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;

Qy	30	GGAGTCCTCTGAGAGGTA	47		
Db	18	GGAGTCGTAGGAGGTA	1		

RESULT 34					
AX473057/c					
LOCUS	AX473057	18 bp	DNA	linear	PAT 09-AUG-2002
DEFINITION	Sequence 6 from Patent WO0220475.				
ACCESSION	AX473057				
VERSION	AX473057.1	GI:22207820			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1				
AUTHORS	Duncan,D.F., Madison,E.L., Semple,J.E., Coombs,G.S., Reiner,J.E.,				
	Ong,E.O. and Araldi,G.L.				
TITLE	Inhibitors of serine protease activity of matrilysin or mtrsl				
JOURNAL	Patent: WO 0220475-A 6 14-MAR-2002;				
	CORVAS INTERNATIONAL, INC. (US)				
FEATURES	Location/Qualifiers				
source	1..18				
	/organism="synthetic construct"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:32630"				
	/note="oligonucleotide primer"				

Query Match	17.1%;	Score 13.2;	DB 1;	Length 18;	
Best Local Similarity	83.3%;	Pred. No. 29;			
Matches	15;	Conservative	0;	Mismatches	3;
				Indels	0;
				Gaps	0;

Qy	30	GGAGTCCTCTGAGAGGTA	47		
Db	18	GGAGTCGTAGGAGGTA	1		

RESULT 35
CO625283
LOCUS AX649089/c 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 10023 from Patent WO0192524.
ACCESSION CO625283
VERSION CO625283.1 GI:41675501
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10023 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 16.9%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCT 39
Db 5 TCTGGAGTCTCTCT 17

RESULT 36
AR466346
LOCUS AX649089/c 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 10023 from patent US 6686188.
ACCESSION AR466346
VERSION AR466346.1 GI:42701403
KEYWORDS Unknown.
SOURCE
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 10023 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES
source 1..17
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

Query Match 16.9%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCT 39
Db 5 TCTGGAGTCTCTCT 17

RESULT 37
AX649089/c
LOCUS AX649089 17 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 929 from Patent EP1273660.
ACCESSION AX649089
VERSION AX649089.1 GI:29151907
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 929 08-JAN-2003;
Aeomica, Inc. (US)
FEATURES
source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 16.6%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 AAGAGCCAGCGAGCT 63
Db 17 ATGAGCCAGCGAGAT 2

RESULT 38
AX762338/c
LOCUS AX762338 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 5659 from Patent WO03040369.
ACCESSION AX762338
VERSION AX762338.1 GI:32256954
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 5659 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 16.6%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AAGACGGCTCTGGGGAT 21
Db 17 AAGGCTGCTGGGGAT 2

RESULT 39
CO625289
LOCUS CO625289 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 10029 from Patent WO0192524.
ACCESSION CO625289
VERSION CO625289.1 GI:41675507
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and

Qy	28	CTGGAGTCCTCTGA	41
Db	4	CTGGAGCCCTCTGA	17
RESULT 42			
AR466352			
LOCUS	AR466352	17 bp	DNA
DEFINITION	Sequence 10029 from patent US 6686188.		linear
ACCESSION	AR466352		
VERSION	AR466352.1	GI:42701409	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 17)		
AUTHORS	Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.B.		
TITLE	Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle		
JOURNAL	Patent: US 6686188-A 10029 03-FEB-2004; Amersham PLC; Buckinghamshire; GB;		
FEATURES	Location/Qualifiers		
source	1..17		
	/organism="unknown"		
	/mol_type="genomic DNA"		
Query Match	16.1%; Score 12.4; DB 1; Length 17;		
Best Local Similarity	92.9%; Pred. No. 38;		
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	29	TGGAGTCCTCTGAG	42
Db	1	TGGAGTCCTCTG	14
RESULT 43			
AX649087/c			
LOCUS	AX649087	17 bp	DNA
DEFINITION	Sequence 927 from Patent EP1273660.		linear
ACCESSION	AX649087		
VERSION	AX649087.1	GI:29151905	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Gu, Y.		
TITLE	Human sodium-hydrogen exchanger like protein 1		
JOURNAL	Patent: EP 1273660-A 927 08-JAN-2003; Aeomica, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1..17		
	/organism="Homo sapiens"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
Query Match	16.1%; Score 12.4; DB 1; Length 17;		
Best Local Similarity	92.9%; Pred. No. 38;		
Matches	13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	50	GAGCCAGCGAGCT	63
Db	17	GAGCCAGCGAGAT	4
RESULT 44			
AX649088/c			
LOCUS	AX649088	17 bp	DNA
			linear
			PAT 22-MAR-2003

```

DEFINITION Sequence 928 from Patent EP1273660.
ACCESSION AX649088
VERSION AX649088.1 GI:29151906
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE 1
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Human sodium-hydrogen exchanger like protein 1
          Patent: EP 1273660-A 928 08-JAN-2003;
          Aeomica, Inc. (US)
FEATURES
    source
        1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 38;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCT 63
Db 16 GAGCCAGCGAAGAT 3

RESULT 45
LOCUS AX649093/c
DEFINITION Sequence 933 from Patent EP1273660.
ACCESSION AX649093
VERSION AX649093.1 GI:29151911
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE 1
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Human sodium-hydrogen exchanger like protein 1
          Patent: EP 1273660-A 933 08-JAN-2003;
          Aeomica, Inc. (US)
FEATURES
    source
        1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 38;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAGAGCCAGCGAA 60
Db 14 AATGAGCCAGCGAA 1

RESULT 46
LOCUS AX734726
DEFINITION Sequence 316 from Patent WO03025177.
ACCESSION AX734726
VERSION AX734726.1 GI:30514003
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
DEFINITION Sequence 928 from Patent EP1273660.
ACCESSION AX649088
VERSION AX649088.1 GI:29151906
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
          reversion, apoptosis and/or resistance to viruses and the use
          thereof as medicaments
JOURNAL Patent: WO 03025177-A 316 27-MAR-2003;
          Molecular Engines Laboratories (FR)
FEATURES
    source
        1..17
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"
Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 38;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCTG 40
Db 3 TCTGGTGTCTCTCTG 16

RESULT 47
LOCUS BD203204/c
DEFINITION Method and reagent for treating diseases or conditions concerning
          molecule participating in vasculogenic response.
ACCESSION BD203204
VERSION BD203204.1 GI:33012974
KEYWORDS JP 2002509721-A/6230.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
TITLE Method and reagent for treating diseases or conditions concerning
          molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 6230 02-APR-2002;
          RIBOSYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
        PN JP 2002509721-A/6230
        PD 02-APR-2002
        PR 24-MAR-1999 JP 2000541291
        PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
        PI JAMES A MCSWIGGEN
        PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
        PC A61P29/00,
        PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
        C12N5/00
        CC Method and reagent for treating diseases or conditions CC
        CC concerning molecule
        CC participating in vasculogenic response
        FH Key Location/Qualifiers
        FT source 1..17
        FT /organism="Homo sapiens (human)".
        FT Location/Qualifiers
        source
            1..17
            /organism="Homo sapiens"
            /mol_type="genomic RNA"
            /db_xref="taxon:9606"
Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 16 GGGGATACACTCTGGA 32
Db 17 GGGGGTATTACTCTGGA 1

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RESULT 48
AX687578/c
LOCUS AX687578 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 310 from Patent EP1281758.
ACCESSION AX687578
VERSION AX687578.1 GI:29410274
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL mdz12
PATENT: EP 1281758-A 310 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCTCTGAGAG 44
Db 17 CTGGAGCCCCCTAGAG 1

RESULT 49
AX727379
LOCUS AX727379 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5066 from Patent WO03025176.
ACCESSION AX727379
VERSION AX727379.1 GI:30506722
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Teitelman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
JOURNAL Medicines
PATENT: WO 03025176-A 5066 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 50 GAGCCAGGAGCTGAT 66
Db 1 GATCCAGGAGCTGAT 17

RESULT 50
CQ858651
LOCUS CQ858651 16 bp DNA linear PAT 31-AUG-2004
DEFINITION Sequence 113 from Patent WO2004069991.
ACCESSION CQ858651

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VERSION CQ858651.1 GI:51852618
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Hansen,B., Thruue,C.A., Petersen,K.D., Westergaard,M. and
Wissenbach,M.
TITLE Oligomeric compounds for the modulation of survivin expression
JOURNAL Patent: WO 2004069991-A 113 19-AUG-2004;
Santaris Pharma A/S (DK)
FEATURES
source
1. .16
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAGGCTG 64
Db 4 CCAGCGAGGCTG 15

RESULT 51
CQ625282
LOCUS CQ625282 17 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 10022 from Patent WO0192524.
ACCESSION CQ625282
VERSION CQ625282.1 GI:41675500
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
Shannon,M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 10022 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 15.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCCTC 38
Db 6 TCTGGAGTCCTC 17

RESULT 52
AR466345
LOCUS AR466345 17 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 10022 from patent US 6686188.
ACCESSION AR466345
VERSION AR466345.1 GI:42701402
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and

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Shannon,M.E.
 Polynucleotide encoding a human myosin-like polypeptide expressed
 predominantly in heart and muscle
 Patent: US 5686188-A 10022 03-FEB-2004;
 Amer sham PLC; Buckinghamshire;
 GBX;

FEATURES
 source
 1. .17
 /location/Qualifiers
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 15.6%; Score 12; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TCTGGAGTCTCTC 38
 Db 6 TCTGGAGTCTCTC 17

RESULT 53
 AR329584/c
 LOCUS AR329584 16 bp RNA linear PAT 17-AUG-2003
 DEFINITION Sequence 6986 from patent US 6566127.
 ACCESSION AR329584
 VERSION AR329584.1 GI:33715392
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6566127-A 6986 20-MAY-2003;
 Ribozyne Pharmaceuticals, Inc. and Chiron Corporation; Boulder, CO
 FEATURES
 source
 1. .16
 /location/Qualifiers
 /organism="unknown"
 /mol_type="unassigned RNA"

Query Match 15.3%; Score 11.8; DB 1; Length 16;
 Best Local Similarity 86.7%; Pred. No. 46;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 52 GCCAGCGAGCTGAT 66
 Db 16 GCCAGCATAGCTGAT 2

RESULT 54
 AR362384/c
 LOCUS AR362384 16 bp DNA linear PAT 03-SEP-2003
 DEFINITION Sequence 12 from patent US 5168062.
 ACCESSION AR362384
 VERSION AR362384.1 GI:34422357
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Stinski,M.F.
 TITLE Transfer vectors and microorganisms containing human
 cytomegalovirus immediate-early promoter-regulatory DNA sequence
 JOURNAL Patent: US 5168062-A 12 01-DEC-1992;
 University of Iowa Research Foundation; Oakdale, IA;
 EPX;

FEATURES
 source
 1. .16
 /location/Qualifiers
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 15.3%; Score 11.8; DB 1; Length 16;

Best Local Similarity 86.7%; Pred. No. 46;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 63 TGATGTCCTGTCAAG 77
 Db 15 TGATGACTGCCAAG 1

RESULT 55
 AR362385/c
 LOCUS AR362385 16 bp DNA linear PAT 03-SEP-2003
 DEFINITION Sequence 13 from patent US 5168062.
 ACCESSION AR362385
 VERSION AR362385.1 GI:34422358
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Stinski,M.F.
 TITLE Transfer vectors and microorganisms containing human
 cytomegalovirus immediate-early promoter-regulatory DNA sequence
 JOURNAL Patent: US 5168062-A 13 01-DEC-1992;
 University of Iowa Research Foundation; Oakdale, IA;
 EPX;

FEATURES
 source
 1. .16
 /location/Qualifiers
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 15.3%; Score 11.8; DB 1; Length 16;
 Best Local Similarity 86.7%; Pred. No. 46;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 63 TGATGTCCTGTCAAG 77
 Db 15 TGATGACTGCCAAG 1

RESULT 56
 AR029815/c
 LOCUS AR029815 16 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 4 from patent US 5861244.
 ACCESSION AR029815
 VERSION AR029815.1 GI:5943029
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Wang,C.-G. and Hepburn,A.G.
 TITLE Genetic sequence assay using DNA triple strand formation
 JOURNAL Patent: US 5861244-A 4 19-JAN-1999;
 Location/Qualifiers
 source
 1. .16
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 14.8%; Score 11.4; DB 1; Length 16;
 Best Local Similarity 92.3%; Pred. No. 53;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 40 GAGAGGTAAAGAG 52
 Db 14 GAGAGGGAAGAG 2

RESULT 57
 BD106403
 LOCUS BD106403 16 bp DNA linear PAT 18-SEP-2002
 DEFINITION Novel LDL-receptor.
 ACCESSION BD106403
 VERSION BD106403.1 GI:23201221

KEYWORDS JP 2002501376-A/418.
SOURCE Chlamydia sp.
ORGANISM Chlamydia sp.
REFERENCE Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
AUTHORS 1 (bases 1 to 16)
Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,
and Hey, P.
TITLE Novel LDI-receptor
JOURNAL Patent: JP 2002501376-A 418 15-JAN-2002;
THE WELLCOME TRUST LTD AS TRUSTEE TO THE WELLCOME TRUST, MERCK & CO
INC
COMMENT PN JP 2002501376-A/418
PD 15-JAN-2002
PF 15-APR-1998 JP 1998543635
PR 15-APR-1997 US 60/043553, 05-JUN-1997 US 60/048740 PI
JOHN ANDREW TODD, JOHN WILFRED HESS, CHARLES
THOMAS CASKEY, ROGER
PI DAVID COX,
PI DAVID GERHOLD, HOLLY HAMMOND, PATRICIA HEY
PC C12N15/12, C12N15/11, C12Q1/68, C07K14/705, C07K16/28, A61K38/17,
PC A61K39/395,
PC A61K48/00
CC Strandedness: Double;
CC Topology: Linear;
PH Key Location/Qualifiers.
FEATURES
source 1. .16
/organism="Chlamydia sp."
/mol_type="genomic DNA"
/db_xref="taxon:35827"
Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 39 TGAGAGGTAAGAGGCC 54
Db 1 TCACAGGTAAGGAGCC 16
RESULT 58
LOCUS I18626 16 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 12 from patent US 5500341.
ACCESSION I18626
VERSION I18626.1 GI:1598981
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
Spear, P.A.
TITLE Species-specific detection of Mycobacterium kansasii
JOURNAL Patent: US 5500341-A 12 19-MAR-1996;
FEATURES
source 1. .16
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 AACACAGCGCGCTGGG 18
Db 1 AACTCGAGCGGCTCGG 16
RESULT 59
LOCUS AR305492 16 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 450 from patent US 6545137.
ACCESSION AR305492

VERSION AR305492.1 GI:31694802
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,
Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,
Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.
TITLE Receptor
JOURNAL Patent: US 6545137-A 450 08-APR-2003;
FEATURES
source 1. .16
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 39 TGAGAGGTAAGAGGCC 54
Db 1 TCACAGGTAAGGAGCC 16
RESULT 60
LOCUS AR309596 16 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 450 from patent US 6555654.
ACCESSION AR309596
VERSION AR309596.1 GI:31701601
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Todd, J.A., Hess, J.W., Caskey, C.T., Cox, R.D., Gerhold, D.,
Hammond, H., Hey, P., Kawaguchi, Y., Merriman, T.R., Metzker, M.L.,
Nakagawa, Y., Phillips, M.S. and Twells, R.C.J.
TITLE LDL-receptor
JOURNAL Patent: US 6555654-A 450 29-APR-2003;
The Wellcome Trust Limited as Trustee for the Wellcome Trust;
London;
WOX;
FEATURES
source 1. .16
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 39 TGAGAGGTAAGAGGCC 54
Db 1 TCACAGGTAAGGAGCC 16
RESULT 61
LOCUS AR455592/c 16 bp RNA linear PAT 20-FEB-2004
DEFINITION Sequence 9 from patent US 6685948.
ACCESSION AR455592
VERSION AR455592.1 GI:42690466
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Zeng, L. and Markoff, L.
TITLE Replication-defective dengue viruses that are replication-defective
JOURNAL in mosquitoes for use as vaccines
Patent: US 6685948-A 9 03-FEB-2004;

The United States of America as represented by the Department of Health and Human Services; Washington, DC;
WOX;

FEATURES
source
Location/Qualifiers
1. .16
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 26 CTCTGGAGTCTCTGA 41
Db 16 CTCTGTGTCTATGA 1

RESULT 62
LOCUS AR630011/c 16 bp DNA linear PAT 14-FEB-2005
DEFINITION Sequence 65 from patent US 6838556.
ACCESSION AR630011
VERSION AR630011.1 GI:59762202
KEYWORDS Unknown.
SOURCE Unknown.

ORGANISM
Unclassified.

REFERENCE 1 (bases 1 to 16)
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Kim,M.Y. and Bruiice,T.W.
TITLE Promoters for regulated gene expression
JOURNAL Patent: US 6838556-A 65 04-JAN-2005;
Genelabs Technologies, Inc.; Redwood City, CA

FEATURES
source
1. .16
/organism="unknown"
/mol_type="genomic DNA"

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAGAGC 53
Db 16 CTGGAGGTGGAGC 1

RESULT 63
AX351113/c
LOCUS AX351113 16 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 65 from Patent WO0194600.
ACCESSION AX351113
VERSION AX351113.1 GI:18616467

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1
AUTHORS Kim,J.P., Starr,D.B., Tam,A.W., Laurance,M.E., Michelotti,E.F.,
Velligan,M.D., Latour,D.R., Thomas,R.L., Kongpachith,A.,
Sheppard,L.T., Lim,M.Y. and Bruiice,T.W.

TITLE Promoters for regulated gene expression
JOURNAL Patent: WO 0194600-A 65 13-DEC-2001;
GENELABS TECHNOLOGIES, INC. (US)

FEATURES
source
1. .16
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAGAGC 53
Db 16 CTGGAGGTGGAGC 1

RESULT 64
AX552593/c
LOCUS AX552593 16 bp RNA linear PAT 27-NOV-2002
DEFINITION Sequence 9 from Patent WO02074963.
ACCESSION AX552593
VERSION AX552593.1 GI:25896602
KEYWORDS West Nile virus (WNV)
SOURCE West Nile virus

ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; Japanese encephalitis virus group.

REFERENCE 1
AUTHORS Markoff,L. and Zeng,L.
TITLE Dengue viruses that are replication defective in mosquitos for use
as vaccines

JOURNAL Patent: WO 02074963-A 9 26-SEP-2002;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES
Location/Qualifiers
source
1. .16

/organism="West Nile virus"
/mol_type="unassigned RNA"
/db_xref="taxon:11082"

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 26 CTCTGGAGTCTCTGA 41
Db 16 CTCTGTGTCTATGA 1

RESULT 65
AX927981/c
LOCUS AX927981 16 bp DNA linear PAT 19-DEC-2003
DEFINITION Sequence 67 from Patent WO03085110.
ACCESSION AX927981
VERSION AX927981.1 GI:40250934

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE 1
AUTHORS Thue,C.A., h G,A.M. and Kristjansen,P.E.
TITLE Oligomeric compounds for the modulation hif-1alpha expression
JOURNAL Patent: WO 03085110-A 67 16-OCT-2003;
Cureon A/S (DK)

FEATURES
Location/Qualifiers
source
1. .16

/organism="synthetic construct"
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/db_xref="taxon:32630"
/notes="Description of Artificial Sequence:antisense
oligonucleotide to human HIP-1a"

Query Match 14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAGC 62
Db 16 AAACACACAGCGAAGC 1

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RESULT 66
AX470971/c
LOCUS AX470971 11 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 548 from Patent WO02053773.
ACCESSION AX470971
VERSION AX470971.1 GI:22206096
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Hofmann,K., Conradt,M. and Petersohn,D.
AUTHORS Method for determining skin stress or skin ageing in vitro
TITLE Patent: WO 02053773-A 548 11-JUL-2002;
JOURNAL HENKEL KGAA (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATCAACTCTG 30
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Db 11 ATCAACTCTG 1

RESULT 67
AX624831/c
LOCUS AX624831 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1872 from Patent WO02053774.
ACCESSION AX624831
VERSION AX624831.1 GI:28452772
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 1872 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
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Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATCAACTCTG 30
|||||
Db 11 ATCAACTCTG 1

RESULT 68
AX632252/c
LOCUS AX632252 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9294 from Patent WO02053774.
ACCESSION AX632252
VERSION AX632252.1 GI:28467867
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9294 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATCAACTCTG 30
|||||
Db 11 ATCAACTCTG 1

RESULT 69
AX587244
LOCUS AX587244 14 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 20 from Patent WO0236761.
ACCESSION AX587244
VERSION AX587244.1 GI:27656109
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 D'Andrea,A.D., Taniguchi,T., Timmers,C. and Grompe,M.
AUTHORS Methods and compositions for the diagnosis of cancer
TITLE susceptibility and defective dna repair mechanisms and treatment
thereof
JOURNAL Patent: WO 0236761-A 20 10-MAY-2002;
FEATURES
source
1. .14
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1. .14
/notes="Intron/Exon Junction of PANCD"

Query Match 14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 AGGTAAGAGC 53
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Db 2 AGGTAAGAGC 12

RESULT 70
BD208921/c
LOCUS BD208921 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD208921
VERSION BD208921.1 GI:33018691
KEYWORDS JP 2002512791-A/2511.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Petersohn,D., Conradt,M. and Hofmann,K.
AUTHORS Method for determining homeostasis of the skin
TITLE Patent: WO 02053774-A 9294 11-JUL-2002;
JOURNAL Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATCAACTCTG 30
|||||
Db 11 ATCAACTCTG 1

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RESULT 69
AX587244
LOCUS AX587244 14 bp DNA linear PAT 10-JAN-2003
DEFINITION Sequence 20 from Patent WO0236761.
ACCESSION AX587244
VERSION AX587244.1 GI:27656109
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 D'Andrea,A.D., Taniguchi,T., Timmers,C. and Grompe,M.
AUTHORS Methods and compositions for the diagnosis of cancer
TITLE susceptibility and defective dna repair mechanisms and treatment
thereof
JOURNAL Patent: WO 0236761-A 20 10-MAY-2002;
FEATURES
source
1. .14
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1. .14
/notes="Intron/Exon Junction of PANCD"

Query Match 14.3%; Score 11; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 AGGTAAGAGC 53
|||||
Db 2 AGGTAAGAGC 12

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RESULT 70
BD208921/c
LOCUS BD208921 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
ACCESSION BD208921
VERSION BD208921.1 GI:33018691
KEYWORDS JP 2002512791-A/2511.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related

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JOURNAL      to hepatitis C virus infection
              Patent: JP 2002512791-A 2511 08-MAY-2002;
COMMENT      RIBOZYME PHARMACEUTICALS INC
OS           Hepatitis virus (hepatitis C virus)
PI           JP 2002512791-A/2511
PD           08-MAY-2002
PF           26-APR-1999 JP 2000545991
PR           27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
PS           25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
PT           LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
FT           PAVCO,
              DENNIS MACEJAK
PC           C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC           A61K37/66,
PC           C12N15/00
CC           Enzymatic nucleic acid treatment of diseases or conditions CC
              related to
CC           hepatitis C virus infection.
FH           Key Location/Qualifiers
FT           1. .15
FT           /organism='Hepatitis virus (hepatitis C FT
              virus)'
              Location/Qualifiers
FEATURES     1. .15
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              /db_xref="taxon:32644"
              14.3%; Score 11; DB 1; Length 15;
Query Match Best Local Similarity 100.0%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GTAAAGAGCCA 55
DB 13 GTAAAGAGCCA 3

RESULT 71
BD208922/c
LOCUS
DEFINITION   Enzymatic nucleic acid treatment of diseases or conditions related
              to hepatitis C virus infection.
ACCESSION   BD208922.1 GI:33018692
VERSION     JP 2002512791-A/2512.
KEYWORDS    unclassified
SOURCE      unclassified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE       Enzymatic nucleic acid treatment of diseases or conditions related
              to hepatitis C virus infection
JOURNAL     RIBOZYME PHARMACEUTICALS INC
COMMENT     Patent: JP 2002512791-A 2512 08-MAY-2002;
OS         Hepatitis virus (hepatitis C virus)
PI         JP 2002512791-A/2512
PD         08-MAY-2002
PF         26-APR-1999 JP 2000545991
PR         27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
PS         25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
PT         LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
FT         PAVCO,
              DENNIS MACEJAK
PC           C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC           A61K37/66,
PC           C12N15/00
CC           Enzymatic nucleic acid treatment of diseases or conditions CC
              related to
CC           hepatitis C virus infection.
FH           Key Location/Qualifiers
FT           1. .15
FT           /organism='Hepatitis virus (hepatitis C FT
              virus)'

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FEATURES     source Location/Qualifiers
              1. .15
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              /db_xref="taxon:32644"
              14.3%; Score 11; DB 1; Length 15;
Query Match Best Local Similarity 100.0%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GTAAAGAGCCA 55
DB 11 GTAAAGAGCCA 1

RESULT 72
A15668/c
LOCUS
DEFINITION   oligonucleotide.
ACCESSION   A15668
VERSION     A15668.1 GI:512155
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
              other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Verrips,C.T., Maat,J., Edens,L. and Ledebor,A.M.
TITLE       Structural genes encoding the various allelic and maturation forms
              of preprothaeumatin, recombinant cloning vehicles comprising said
              structural genes and expression thereof in transformed microbial
              host cells
              Patent: EP 0054331-A 4 23-JUN-1982;
              UNILEVER NV; UNILEVER PLC
JOURNAL     UNILEVER NV; UNILEVER PLC
FEATURES     source Location/Qualifiers
              1. .14
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              14.0%; Score 10.8; DB 1; Length 14;
Query Match Best Local Similarity 85.7%; Pred. No. 61;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 56 GCGAAGCTGATGTC 69
DB 14 GCGAAGCTGACGCC 1

RESULT 73
A15684
LOCUS
DEFINITION   oligonucleotide.
ACCESSION   A15684
VERSION     A15684.1 GI:512743
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    synthetic construct
              other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Verrips,C.T., Maat,J., Edens,L. and Ledebor,A.M.
TITLE       Structural genes encoding the various allelic and maturation forms
              of preprothaeumatin, recombinant cloning vehicles comprising said
              structural genes and expression thereof in transformed microbial
              host cells
              Patent: EP 0054331-A 20 23-JUN-1982;
              UNILEVER NV; UNILEVER PLC
JOURNAL     UNILEVER NV; UNILEVER PLC
FEATURES     source Location/Qualifiers
              1. .15
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              14.0%; Score 10.8; DB 1; Length 15;
Query Match

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Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 56 GCGAAGCTGATGTC 69
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Db 1 GCGAAGCTGAAGGC 14

RESULT 74
AR033420/c
LOCUS AR033420 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 186 from patent US 5869253.
ACCESSION AR033420
VERSION AR033420.1 GI:5949025
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 5869253-A 186 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTC 70
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Db 15 CCAAGATGATGTC 2

RESULT 75
AR113242/c
LOCUS AR113242 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 186 from patent US 6132966.
ACCESSION AR113242
VERSION AR113242.1 GI:14093564
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Method and reagent for inhibiting hepatitis C virus replication
JOURNAL Patent: US 6132966-A 186 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTC 70
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Db 15 CCAAGATGATGTC 2

RESULT 76
BD207153/c
LOCUS BD207153 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD207153
VERSION BD207153.1 GI:33016923
KEYWORDS JP 2002512791-A/743.
SOURCE unidentified

ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 743 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/743
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
/organism="Hepatitis virus (hepatitis C virus)"
/mol_type="unassigned DNA"

Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTC 70
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Db 15 CCAAGATGATGTC 2

RESULT 77
CS004710/c
LOCUS CS004710 15 bp DNA linear PAT 07-FEB-2005
DEFINITION Sequence 2738 from Patent EP1502950.
ACCESSION CS004710
VERSION CS004710.1 GI:58740065
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1
AUTHORS Stinchcomb,D.T., Chowrira,B., Drenzo,A., Draper,K.G., Dudycz,L.W., Grimm,S., Karpeisky,A., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method for purifying chemically modified RNA
JOURNAL Patent: EP 1502950-A 2738 02-FEB-2005;
RIBOZYME Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..15
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 25 ACTCTGATGTC 38
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Db      14 ACTCTGAAGTCTTC 1

RESULT 78
CS004712/c
LOCUS      15 bp      DNA      linear      PAT 07-FEB-2005
DEFINITION Sequence 2740 from Patent EPI502950.
ACCESSION CS004712
VERSION    CS004712.1 GI:58740067
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
           unclassified.
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Chowrira,B., Direnzo,A., Draper,K.G., Dudycz,L.W.,
           Grimm,S., Karpeisky,A., Kisich,K., Matulic-Adamic,J.,
           McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
           Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
           Woolf,T.
TITLE      Method for purifying chemically modified RNA
JOURNAL    Patent: EP 1502950-A 2740 02-FEB-2005;
           Ribozyme Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
           source
             1..15
               /organism="unidentified"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32644"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTCTTC 38
Db      14 ACTCTGAAGTCTTC 1

RESULT 79
CS005312
LOCUS      15 bp      DNA      linear      PAT 07-FEB-2005
DEFINITION Sequence 3340 from Patent EPI502950.
ACCESSION CS005312
VERSION    CS005312.1 GI:58740667
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
           unclassified.
REFERENCE  1
AUTHORS    Stinchcomb,D.T., Chowrira,B., Direnzo,A., Draper,K.G., Dudycz,L.W.,
           Grimm,S., Karpeisky,A., Kisich,K., Matulic-Adamic,J.,
           McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
           Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
           Woolf,T.
TITLE      Method for purifying chemically modified RNA
JOURNAL    Patent: EP 1502950-A 3340 02-FEB-2005;
           Ribozyme Pharmaceuticals, Inc. (US)
FEATURES   Location/Qualifiers
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Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      29 TGGAGTCTCTTGAG 42
Db      2 TGGAGTACCTTGAG 15

RESULT 80
I39319/c
LOCUS      15 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 357 from patent US 5616488.
ACCESSION I39319
VERSION    I39319.1 GI:2083799
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE      IL-5 targeted ribozymes
JOURNAL    Patent: US 5616488-A 357 01-APR-1997;
           Location/Qualifiers
           source
             1..15
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTCTTC 38
Db      14 ACTCTGAAGTCTTC 1

RESULT 81
I39320/c
LOCUS      15 bp      DNA      linear      PAT 13-MAY-1997
DEFINITION Sequence 358 from patent US 5616488.
ACCESSION I39320
VERSION    I39320.1 GI:2083800
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE      IL-5 targeted ribozymes
JOURNAL    Patent: US 5616488-A 358 01-APR-1997;
           Location/Qualifiers
           source
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               /mol_type="unassigned DNA"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTCTTC 38
Db      14 ACTCTGAAGTCTTC 1

RESULT 82
I57649/c
LOCUS      15 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 186 from patent US 5610054.
ACCESSION I57649
VERSION    I57649.1 GI:2482713
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Draper,K.G.
TITLE      Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL    Patent: US 5610054-A 186 11-MAR-1997;
           Location/Qualifiers
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Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGTC 70
Db 15 CCAAGATGATGTC 2

RESULT 83
LOCUS I61819
DEFINITION Sequence 373 from patent US 5658780.
ACCESSION I61819
VERSION I61819.1 GI:2479767
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Real a targeted ribozymes
JOURNAL Patent: US 5658780-A 373 19-AUG-1997;
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                /mol_type="unassigned DNA"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAG 42
Db 2 TGGAGTACCTGAG 15

RESULT 84
AX635599/c
LOCUS AX635599
DEFINITION Sequence 2738 from Patent EPI260586.
ACCESSION AX635599
VERSION AX635599.1 GI:28471213
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 2738 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 ACTCTGGAGTCCTC 38
Db 14 ACTCTGAAGTCCTC 1

RESULT 85
AX635601/c
LOCUS AX635601
DEFINITION Sequence 2740 from Patent EPI260586.
ACCESSION AX635601
VERSION AX635601.1 GI:28471215
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 2740 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAG 42
Db 2 TGGAGTACCTGAG 15

RESULT 87
AR035176
LOCUS AR035176
DEFINITION Sequence 36 from patent US 5871730.

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AX635601/c
LOCUS AX635601
DEFINITION Sequence 2740 from Patent EPI260586.
ACCESSION AX635601
VERSION AX635601.1 GI:28471215
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 2740 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 ACTCTGGAGTCCTC 38
Db 14 ACTCTGAAGTCCTC 1

RESULT 86
AX636201
LOCUS AX636201
DEFINITION Sequence 3340 from Patent EPI260586.
ACCESSION AX636201
VERSION AX636201.1 GI:28471815
KEYWORDS
SOURCE unidentified
ORGANISM unclassified sequences.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 3340 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
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                /mol_type="unassigned RNA"
                /db_xref="taxon:32644"

Query Match      14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAG 42
Db 2 TGGAGTACCTGAG 15

RESULT 87
AR035176
LOCUS AR035176
DEFINITION Sequence 36 from patent US 5871730.

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ACCESSION AR035176
VERSION AR035176.1 GI:5951844
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Brzezinski,R., Dery,C.V. and Beaulieu,C.
TITLE Thermostable xylanase DNA, protein and methods of use
JOURNAL Patent: US 5871730-A 36 16-FEB-1999;
FEATURES
    source
        Location/Qualifiers
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                /mol_type="unassigned DNA"
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 68;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 56 GCGAAGCTGATG 67
Db 2 GCGAGCTGATG 13
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RESULT 88
BD263782 13 bp RNA linear PAT 17-JUL-2003
LOCUS Adeno-associated virus-delivered ribozyme compositions and methods
DEFINITION of use.
ACCESSION BD263782
VERSION BD263782.1 GI:33073550
KEYWORDS JP 2002542805-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 13)
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods
of use
JOURNAL Patent: JP 2002542805-A 4 17-DEC-2002;
UNIVERSITY OF FLORIDA
COMMENT OS Artificial Sequence
PN JP 2002542805-A/4
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615402
PR 30-APR-1999 US 60/131942
PI ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
,CHRISTIAN TESCHENDORF,
PI CORINNA BURGER
PC C12N15/09 A01K67/027,C12N9/00,C12Q1/68 C12N15/00 CC
Description of Artificial Sequence: SYNTHETIC PEPTIDE FH Key
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        FT /organism='Artificial Sequence'.
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                /mol_type="genomic RNA"
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Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 68;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTG 40
Db 1 TGGAGTCCGCTG 12
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RESULT 89
AX048268 13 bp RNA linear PAT 15-DEC-2000
LOCUS Adeno-associated virus-delivered ribozyme compositions and methods
DEFINITION of use.
ACCESSION BD263782
VERSION BD263782.1 GI:33073550
KEYWORDS JP 2002542805-A/4.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 13)
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods
of use
JOURNAL Patent: JP 2002542805-A 4 17-DEC-2002;
UNIVERSITY OF FLORIDA
COMMENT OS Artificial Sequence
PN JP 2002542805-A/4
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615402
PR 30-APR-1999 US 60/131942
PI ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
,CHRISTIAN TESCHENDORF,
PI CORINNA BURGER
PC C12N15/09 A01K67/027,C12N9/00,C12Q1/68 C12N15/00 CC
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Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 68;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTG 40
Db 1 TGGAGTCCGCTG 12
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DEFINITION Sequence 4 from Patent WO0066780.
ACCESSION AX048268
VERSION AX048268.1 GI:11877033
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods
of use
JOURNAL Patent: WO 0066780-A 4 09-NOV-2000;
FEATURES
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Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 68;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTG 40
Db 1 TGGAGTCCGCTG 12
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RESULT 90
BD209276 14 bp RNA linear PAT 17-JUL-2003
LOCUS Enzymatic nucleic acid treatment of diseases or conditions related
DEFINITION to hepatitis C virus infection.
ACCESSION BD209276
VERSION BD209276.1 GI:33019046
KEYWORDS JP 2002512791-A/2866.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2866 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2866
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions
related to
hepatitis C virus infection.
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Query Match 13.5%; Score 10.4; DB 1; Length 14;

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Best Local Similarity 91.7%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 62 CTGATGTCCTGT 73
Db 1 CTGCTGTCCTGT 12

RESULT 91
LOCUS A52274 10 bp DNA linear PAT 12-DEC-1997
DEFINITION Sequence 64 from Patent EP0705842.
ACCESSION A52274
VERSION A52274.1 GI:2852038
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Bartnik,B.D. and Margerie,D.D.
TITLE Regulated genes by stimulation of chondrocytes with 1L-1beta
JOURNAL Patent: EP 0705842-A 64 10-APR-1996;
COMMENT HOECHST AG (DE)
Other publication ZA 9508381 960424
Other publication JP 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 92
LOCUS A91804 10 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 3 from Patent WO9823775.
ACCESSION A91804
VERSION A91804.1 GI:6740684
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Nees,M. and Duerst,M.
TITLE DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
JOURNAL Patent: WO 9823775-A 3 04-JUN-1998;
DEUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)
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Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 93
LOCUS A97598 10 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 4 from Patent WO9915680.
ACCESSION A97598
VERSION A97598.1 GI:6780901
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Roberts,J.A. and Paul,W.
TITLE CONTROL OF PLANT ABSCISSION AND POD DEHISCENCE OR SHATTER
JOURNAL Patent: WO 9915680-A 4 01-APR-1999;
BIOGEMMA UK LIMITED (GB); ROBERTS JEREMY ALAN (GB)
FEATURES
source
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 94
LOCUS AR016246 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 14 from patent US 5776683.
ACCESSION AR016246
VERSION AR016246.1 GI:3972523
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Smith,H.S. and Chen,L.-C.
TITLE Methods for identifying genes amplified in cancer cells
JOURNAL Patent: US 5776683-A 14 07-JUL-1998;
FEATURES
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 95
LOCUS AR044027 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5817461.
ACCESSION AR044027
VERSION AR044027.1 GI:5965492
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Austin,R.C., Hirsh,J. and Weitz,J.I.
TITLE Methods and compositions for diagnosis of hyperhomocysteinemia
JOURNAL Patent: US 5817461-A 4 06-OCT-1998;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 96
LOCUS AR079092
DEFINITION Sequence 13 from patent US 5965409.
ACCESSION AR079092
VERSION AR079092.1 GI:10005838
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Pardue,A.B. and Liang,P.
TITLE System for comparing levels or amounts of mRNAs
JOURNAL Patent: US 5965409-A 13 12-OCT-1999;
FEATURES
source
Location/Qualifiers
1..10
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 97
LOCUS AR079528
DEFINITION Sequence 3 from patent US 5965707.
ACCESSION AR079528
VERSION AR079528.1 GI:10006272
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Tam,S.-Y., Tsai,M. and Galli,S.J.
TITLE Rln2, a novel inhibitor of Ras-mediated signaling
JOURNAL Patent: US 5965707-A 3 12-OCT-1999;
FEATURES
source
Location/Qualifiers
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Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 98
LOCUS AR099718
DEFINITION Sequence 28 from patent US 6077948.
ACCESSION AR099718

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Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 99
LOCUS AR113051
DEFINITION Sequence 4 from patent US 6132965.
ACCESSION AR113051
VERSION AR113051.1 GI:14093373
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Austin,R.C., Hirsh,J. and Weitz,J.I.
TITLE Methods and compositions for diagnosis of hyperhomocysteinemia
JOURNAL Patent: US 6132965-A 4 17-OCT-2000;
FEATURES
source
Location/Qualifiers
1..10
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 100
LOCUS BD107610
DEFINITION Novel microsatellite DNA derived from pear plants and method for discriminating pear plants using the same.
ACCESSION BD107610
VERSION BD107610.1 GI:23202428
KEYWORDS JP 2002034597-A/19.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Yamamoto,T., Sawamura,Y., Imai,T., Matsuda,N., Saito,T., Shoda,M.,
Kotobuki,K., Hayashi,K., Ba,Y., Kozono,M. and Kimura,T.
TITLE Novel microsatellite DNA derived from pear plants and method for discriminating pear plants using the same
JOURNAL Patent: JP 2002034597-A 19 05-FEB-2002;
COMMENT FRUIT TREE RES STATION
OS Artificial Sequence
FN JP 2002034597-A/19
PD 05-FEB-2002

/organism="unknown"
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 100
LOCUS BD107610
DEFINITION Novel microsatellite DNA derived from pear plants and method for discriminating pear plants using the same.
ACCESSION BD107610
VERSION BD107610.1 GI:23202428
KEYWORDS JP 2002034597-A/19.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Yamamoto,T., Sawamura,Y., Imai,T., Matsuda,N., Saito,T., Shoda,M.,
Kotobuki,K., Hayashi,K., Ba,Y., Kozono,M. and Kimura,T.
TITLE Novel microsatellite DNA derived from pear plants and method for discriminating pear plants using the same
JOURNAL Patent: JP 2002034597-A 19 05-FEB-2002;
COMMENT FRUIT TREE RES STATION
OS Artificial Sequence
FN JP 2002034597-A/19
PD 05-FEB-2002
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PF 21-JUL-2000 JP 2000220339
PI TOSHIYA YAMAMOTO,TUTAKA SAWAMURA,TSUYOSHI IMAI,NAGAO MATSUDA,
PI TOSHIHIRO SAITO,MORIYUKI SHODA,KAZUO KOTOBUKI,KENKI HAYASHI,
PI YOSHIYUKI BAN,
PI MASANORI KOZONO,TETSUYA KIMURA
PC C12N1/69,A01H1/00,C12N15/09,C12N15/00
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FT source 1..10
    Location/Qualifiers
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Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||||
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RESULT 101
BD240697
LOCUS BD240697 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240697
VERSION BD240697.1 GI:33050467
KEYWORDS JP 2002534056-A/2115.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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    Homnidae; Homo.
REFERENCE
    1 (bases 1 to 10)
    Roberts,B.L. and Shankara,S.
    Preparation and use of superior vaccines
    Patent: JP 2002534056-A 2115 15-OCT-2002;
    GENZYME CORP
COMMENT
    OS Homo sapiens (human)
    PN JP 2002534056-A/2115
    PD 15-OCT-2002
    PF 18-JUN-1998 JP 2000554749
    PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
    19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
    19-JUN-1998 US 60/089927,19-JUN-1998 US 60/090079 PR
    19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
    19-JUN-1998 US 60/089922,19-JUN-1998 US 60/090072 PR
    19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
    19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
    19-JUN-1998 US 60/089959,19-JUN-1998 US 60/090043 PR
    19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
    19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
    19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
    19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
    19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
    08-DEC-1998 US 60/111715
    PI BRUCE L ROBERTS,GRINIVAS SHANKARA
    PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
    C12N1/19,
    PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
    G01N37/00,
    PC C12N15/00,C12N5/00,C12N15/00
    CC Preparation and use of superior vaccines
    FH Key Location/Qualifiers
    FT source 1..10
        /organism="Homo sapiens (human)".
        Location/Qualifiers
FEATURES
    source
        1..10
        /organism="unknown"

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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 ACAAGACGGC 13
Db 1 ACAAGACGGC 10
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    |||||
RESULT 102
BD248338
LOCUS BD248338 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Tobacco-origin novel salicylic acid-inducible gene and promoter.
ACCESSION BD248338
VERSION BD248338.1 GI:33058108
KEYWORDS JP 2002524051-A/14.
SOURCE synthetic construct
ORGANISM synthetic construct
    other sequences; artificial sequences.
REFERENCE
    1 (bases 1 to 10)
    Stuijver,M.H., Jepson,I., Horvath,D.M. and Chua,N.H.
    Tobacco-origin novel salicylic acid-inducible gene and promoter
    Patent: JP 2002524051-A 14 06-AUG-2002;
    SYNGENTA MOGEN BV
COMMENT
    OS Artificial Sequence
    PN JP 2002524051-A/14
    PD 06-AUG-2002
    PF 02-AUG-1999 JP 2000563809
    PR 03-AUG-1998 US 60/095187
    PI MAARTEN HENDRIK STUIJVER,IAN JEPSON,DIANA MEREDITH HORVATH,NAM
    PI HAI CHUA
    PC C12N15/09,A01H5/00,C12N5/10,C12N15/00,C12N5/00 CC
    Description of Artificial Sequence Primer API FH Key
    Location/Qualifiers
    FT source 1..10
        /organism="Artificial Sequence".
        Location/Qualifiers
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    source
        1..10
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10
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    |||||
    |||||
    |||||
RESULT 103
LOCUS I22447
DEFINITION Sequence 28 from patent US 5527884.
ACCESSION I22447
VERSION I22447.1 GI:1602801
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 10)
    Russell,M.S. and Utans,U.
    Mediators of chronic allograft rejection and DNA molecules encoding
    them
    Patent: US 5527884-A 28 18-JUN-1996;
    JOURNAL Location/Qualifiers
FEATURES
    source
        1..10
        /organism="unknown"

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/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
        |||||
        |

RESULT 104
LOCUS      I34793
DEFINITION Sequence 13 from patent US 5599672.
ACCESSION  I34793
VERSION     I34793.1 GI:2087761
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Liang,P., Pardee,A.B. and Bianchi,C.F.
TITLE       Method of differential display of exposed mRNA by RT/PCR
JOURNAL     Patent: US 5599672-A 13 04-FEB-1997;
FEATURES
source      1. .10
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
        |||||
        |

RESULT 105
LOCUS      I64511
DEFINITION Sequence 13 from patent US 5665547.
ACCESSION  I64511
VERSION     I64511.1 GI:2481405
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Pardee,A.B. and Liang,P.
TITLE       Methods of comparing levels or amounts of mRNAs
JOURNAL     Patent: US 5665547-A 13 09-SEP-1997;
FEATURES
source      1. .10
/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
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RESULT 106
LOCUS      AR238724
DEFINITION Sequence 132 from patent US 6468743.
ACCESSION  AR238724
VERSION     AR238724.1 GI:27283794

/mol_type="unassigned DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
        |||||
        |

RESULT 107
LOCUS      AR270938
DEFINITION Sequence 3 from patent US 6500942.
ACCESSION  AR270938
VERSION     AR270938.1 GI:29702188
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Tam,S.-Y., Tsai,M. and Galli,S.J.
TITLE       Kin2, a novel inhibitor of Ras-mediated signaling
JOURNAL     Patent: US 6500942-A 3 31-DEC-2002;
            Beth Israel Deaconess Medical Center and The Board of Trustees of
            the Leland Stanford, Jr., University; Palo Alto, CA

FEATURES
source      1. .10
/mol_type="genomic DNA"

Query Match      13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      51 AGCCAGCGAA 60
Db      1 AGCCAGCGAA 10
        |||||
        |

RESULT 108
LOCUS      AX016299
DEFINITION Sequence 2 from Patent WO9949046.
ACCESSION  AX016299
VERSION     AX016299.1 GI:10041862
KEYWORDS
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM
REFERENCE   1
AUTHORS     Roberts,J.A., Wyatt,P. and Whitelaw,C.
TITLE       Signal transduction protein involved in plant dehiscence
JOURNAL     Patent: WO 9949046-A 2 30-SEP-1999;
            ROBERTS JEREMY ALAN (GB); BIOEMMA UK LTD (GB); WYATT PAUL (GB);
            WHITELAW CATHERINE (GB)

FEATURES
source      1. .10
/mol_type="synthetic construct"
/mol_type="unassigned DNA"

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/db_xref="taxon:32630"
/notes="Arbitrary primer A"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
   |||||
Db 1 AGCCAGCGAA 10

RESULT 109
AX152307/c
LOCUS AX152307 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 222 from Patent WO0138577.
ACCESSION AX152307
VERSION AX152307.1 GI:14533958
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
Vuculescu,V.B., Vogelstein,B. and Kinzler,K.W.
AUTHORS Human transcriptomes
TITLE Patent: WO 0138577-A 222 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGGCTGGGG 19
   |||||
Db 10 CGGCTGGGG 1

RESULT 110
BD023238
LOCUS BD023238 10 bp DNA linear PAT 27-AUG-2002
DEFINITION DNA for evaluating progress potential of cervical diseases.
ACCESSION BD023238
VERSION BD023238.1 GI:22564461
KEYWORDS JP 2001504703-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Durst,M. and Ness,M.
TITLE DNA for evaluating progress potential of cervical diseases
JOURNAL Patent: JP 2001504703-A 3 10-APR-2001;
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES EFFENTLICHEN RECHTS
COMMENT PN JP 2001504703-A/3
PD 10-APR-2001
PF 12-NOV-1997 JP 1998524127
PR 27-NOV-1996 DE 19649207.6
PI MATHIAS DURST,MATHIAS NESS
PC C12N15/09,C07K14/00,C07K16/00,C12P21/02,C12Q1/68,C12Q1/70, PC
G01N33/574,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC /desc = 'Primer'
FH Key Location/Qualifiers.

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FEATURES
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
   |||||
Db 1 AGCCAGCGAA 10

RESULT 111
AR641426
LOCUS AR641426 13 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 14 from patent US 6861057.
ACCESSION AR641426
VERSION AR641426.1 GI:62776633
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Gaudernack,G., Eriksen,J.A. and Moller,M.
TITLE Immunogenic .beta.-amyloid peptide
JOURNAL Patent: US 6861057-A 14 01-MAR-2005;
GenVex AS; Oslo;
NOX;

FEATURES
source
1. .13
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 TCTGAGAGGT 46
   |||||
Db 1 TCTGAGAGGT 10

RESULT 112
AR051174/c
LOCUS AR051174 14 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5830654.
ACCESSION AR051174
VERSION AR051174.1 GI:5974538
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Millman,C.I.
TITLE Nucleic acid probes to Haemophilus influenzae
JOURNAL Patent: US 5830654-A 2 03-NOV-1998;
FEATURES
source
1. .14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 13.0%; Score 10; DB 1; Length 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 AGCGAGAGCTG 64
   |||||
Db 12 AGCGAGAGCTG 3

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RESULT 113
BD068997/c
LOCUS
DEFINITION
Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors.
ACCESSION
BD068997
VERSION
BD068997.1 GI:22614600
KEYWORDS
JP 2001511003-A/1837.
SOURCE
unidentified
ORGANISM
unclassified.
1 (bases 1 to 14)
REFERENCE
AUTHORS
Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE
Enzymatic nucleic acid treatment of diseases or conditions related
to levels of epidermal growth factor receptors
JOURNAL
Patent: JP 2001511003-A 1837 07-AUG-2001;
RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT
OS Unidentified
PN JP 2001511003-A/1837
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PI
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Unidentified'.
FEATURES
source
1..14
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'
Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 49 AGAGCCAGCG 58
|||||
DB 14 AGAGCCAGCG 5
RESULT 114
BD197865/c
LOCUS
DEFINITION
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION
BD197865
VERSION
BD197865.1 GI:33007635
KEYWORDS
JP 2002509721-A/891.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 14)
REFERENCE
AUTHORS
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and McSwiggen,J.A.
TITLE
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL
Patent: JP 2002509721-A 891 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Homo sapiens (human)
PN JP 2002509721-A/891
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN

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PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00/A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Homo sapiens (human)'.
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source
1..14
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'
Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 58 GAGCTGATG 67
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DB 10 GAGCTGATG 1
RESULT 115
I15960/c
LOCUS
DEFINITION
Sequence 2 from patent US 5472843.
ACCESSION
I15960
VERSION
I15960.1 GI:1250868
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Milliman,C.L.
TITLE
Nucleic acid probes to Haemophilus influenzae
JOURNAL
Patent: US 5472843-A 2 05-DEC-1995;
FEATURES
Location/Qualifiers
source
1..14
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 55 AGCGAAGCTG 64
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DB 12 AGCGAAGCTG 3
RESULT 116
AR403497/c
LOCUS
DEFINITION
Sequence 1837 from patent US 6623962.
ACCESSION
AR403497
VERSION
AR403497.1 GI:40150947
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS
Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE
Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL
Patent: US 6623962-A 1837 23-SEP-2003;
Sirma Therapeutics, Inc. and Aston University; Boulder, CO
FEATURES
Location/Qualifiers
source
1..14
/organism='unknown'

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/mol_type="genomic DNA"

Query Match      13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 AGAGCCAGCG 58
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Db 14 AGAGCCAGCG 5

RESULT 117
AR069833/c
LOCUS AR069833 13 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 49 from patent US 5891685.
ACCESSION AR069833
VERSION AR069833.1 GI:7220721
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Yamagishi,M., Takai,Y., Mikawa,T., Hara,M., Ueda,M. and Ohara,A.
TITLE Method for producing ester of
(s)- gamma -halogenated- beta -hydroxybutyric acid
JOURNAL Patent: US 5891685-A 49 08-APR-1999;
FEATURES Location/Qualifiers
          source
            1..13
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 60 AGCTGATGTCCTG 72
    |||||
Db 13 AGCTGATGACTTG 1

RESULT 118
E15186/c
LOCUS E15186 13 bp DNA linear PAT 28-JUL-1999
DEFINITION Selenophoma donacis CBS417.51 - specific sequence in 16S rRNA gene.
ACCESSION E15186
VERSION E15186.1 GI:5709869
KEYWORDS JP 1998052290-A/19.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 13)
AUTHORS Yamagishi,M., Takai,Y., Mikawa,T., Oohara,A., Hara,M. and Ueda,M.
TITLE PRODUCTION OF (S)-GAMMA-HALOGENATED-BETA-HYDROXYLACTIC ACID ESTER
JOURNAL Patent: JP 1998052290-A 19 24-FEB-1998;
COMMENT MITSUBISHI CHEM CORP
OS Selenophoma donacis
PN JP 1998052290-A/19
PD 24-FEB-1998
PF 03-JUN-1997 JP 1997145613
PR 03-JUN-1996 JP 96P 140087
PI YAMAGISHI MASAHIRO, TAKAI YUKIE, MIKAWA TAKASHI, OOHARA AKIKO,
PI HARA MARI,
PI UEDA MAKOTO
PC C12P7/62, (C12P7/62, C12R1:645);
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT source 1..13
   /organism='Selenophoma donacis' FT
   /strain='CBS417.51',
   Location/Qualifiers
   1..13

RESULT 119
AR06943/c
LOCUS AR06943 13 bp DNA linear PAT 02-DEC-1994
DEFINITION Sequence 2 from Patent EP 0314161.
ACCESSION AR06943
VERSION AR06943.1 GI:590397
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Harris,L.J., Lipsich,L.A. and Walls,M.A.
TITLE Human immunoglobulines produced by recombinant DNA techniques
JOURNAL Patent: EP 0314161-A1 2 03-MAY-1989;
FEATURES Location/Qualifiers
          source
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              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 64 GATGTCTCTGTCAC 76
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Db 13 GATGTACTGCCAA 1

RESULT 120
AR196782/c
LOCUS AR196782 13 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1247 from patent US 6350934.
ACCESSION AR196782
VERSION AR196782.1 GI:20246219
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Zwick,M.G., Edington,B.E., McSwiggen,J.A., Merlo,P. Ann Owens.,
Gao,L., Skokut,T.A., Young,S.A., Folkerts,O. and Merlo,D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 1247 26-FEB-2002;
FEATURES Location/Qualifiers
          source
            1..13
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 85;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCCTC 38
    |||||
Db 13 CTCTAGAGTCCCC 1

RESULT 121
AR027402/c
LOCUS AR027402 14 bp DNA linear PAT 29-SEP-1999

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[illegible]


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Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
TITLE HIV nef targeted ribozymes
JOURNAL Patent: US 5972704-A 49 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..14
/mol_type="unassigned DNA"
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71
Db 14 AAGCTGGTGTTCT 2

RESULT 127
AR120747/c
LOCUS AR120747 14 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 49 from patent US 6159692.
ACCESSION AR120747
VERSION AR120747.1 GI:14104323
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and Thompson,J.D.
TITLE Method and reagent for inhibiting human immunodeficiency virus replication
JOURNAL Patent: US 6159692-A 49 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..14
/mol_type="unassigned DNA"
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71
Db 14 AAGCTGGTGTTCT 2

RESULT 128
AR164788
LOCUS AR164788 14 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 99 from patent US 6274332.
ACCESSION AR164788
VERSION AR164788.1 GI:16237972
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE Mutations in the KCNE1 gene encoding human minK which cause arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
JOURNAL Patent: US 6274332-A 99 14-AUG-2001;
FEATURES Location/Qualifiers
source 1..14
/mol_type="unassigned DNA"
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 129
BD068929
LOCUS BD068929 14 bp RNA linear PAT 27-AUG-2002
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors.
ACCESSION BD068929
VERSION BD068929.1 GI:22614532
KEYWORDS
SOURCE JP 2001511003-A/1769.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Akhtar,S., Fell,P. and Mcswiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: JP 2001511003-A 1769 07-AUG-2001;
COMMENT RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
OS Unidentified
PN JP 2001511003-A/1769
PD 07-AUG-2001
PF 14-JAN-1998 JP 1998532913
PR 31-JAN-1997 US 60/036476,04-DEC-1997 US 08/985162 PT
SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
C12N9/00,C07K14/71
CC Strandedness: Single;
CC Topology: Linear;
CC Enzymatic nucleic acid treatment of diseases or conditions CC related to
CC levels of epidermal growth factor receptors
FH Key Location/Qualifiers
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FT /organism='Unidentified'.
FEATURES Location/Qualifiers
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/db_xref="taxon:32644"
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GACGGCCTGGGGA 20
Db 2 GACGGCCGGGCA 14

RESULT 130
BD209346
LOCUS BD209346 14 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD209346
VERSION BD209346.1 GI:33019116
KEYWORDS
SOURCE JP 2002512791-A/2936.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2936 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2936
PD 08-MAY-2002

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PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
FAVCO, DENNIS MACEJAK
PI C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC C12N9/00,A61K37/66,
PC A61K37/66,
PC C12N15/00,
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..14
FT virus),
/organism='Hepatitis virus (hepatitis C FT
virus)',
Location/Qualifiers
source 1..14
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GACGGCTGGGGA 20
|||||
Db 2 GACGGCTGGGGA 14

RESULT 131
LOCUS BD222899 14 bp DNA linear PAT 17-JUL-2003
DEFINITION KVLQ1-QT extension syndrome.
ACCESSION BD222899
VERSION BD222899.1 GI:33032669
KEYWORDS JP 2002521045-A/97,
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 14)
AUTHORS Keating,M.T., Sanguinetti,M.C., Karan,M.E., Landes,G.M.,
Connors,T.D., Burn,T.C. and Splawski,I.
TITLE KVLQ1-QT extension syndrome
JOURNAL Patent: JP 2002521045-A 97 16-JUL-2002;
UNIVERSITY OF UTAH RESEARCH FOUNDATION,GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002521045-A/97
PD 16-JUL-2002
PF 12-MAY-1999 JP 2000562052
PR 29-JUL-1998 US 60/094477,17-AUG-1998 US 09/135010 PI
MARK T KEATING,MICHAEL C SANGUINETTI,MARK E KARAN,GREGORY M PI
LANDES.
PI TIMOTHY D CONNORS,TIMOTHY C BURN,IGOR SPLAWSKI PC
C12N15/09,A01K67/027,C07K14/46,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/08,C12Q1/02,C12Q1/68,G01N33/15,G01N33/ PC
50, G01N33/53,G01N33/53,G01N33/566,G01N33/577,G01N33/58,G01N33/68,
PC C12N15/00,
PC C12N5/00
CC KVLQ1-QT extension syndrome
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
/organism='Homo sapiens'
/mol_type='genomic DNA'

FEATURES
source 1..14
Location/Qualifiers

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/db_xref='taxon:9606'

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGGT 46
|||||
Db 2 TCCTTTAAGAGGT 14

RESULT 132
LOCUS I32082 14 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 26 from patent US 5585238.
ACCESSION I32082
VERSION I32082.1 GI:1822873
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Ligon,J.M. and Beck,J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5585238-A 26 17-DEC-1996;
FEATURES Location/Qualifiers
source 1..14
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGGG 19
|||||
Db 13 AGACGGCTCCGG 1

RESULT 133
LOCUS I78251 14 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 49 from patent US 5693535.
ACCESSION I78251
VERSION I78251.1 GI:3014405
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Draper,K.G., Chowrira,B., McSwiggen,J., Stinchcomb,D.T. and
Thompson,J.D.
TITLE HIV targeted ribozymes
JOURNAL Patent: US 5693535-A 49 02-DEC-1997;
FEATURES Location/Qualifiers
source 1..14
/organism='unknown'
/mol_type='unassigned DNA'

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AGCTGATGTCCT 71
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Db 14 AGCTGGTGTCT 2

RESULT 134
LOCUS AR179956 14 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 24 from patent US 633152.
ACCESSION AR179956

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VERSION      AR179956.1  GI:20221989
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE        Gene expression profiles in normal and cancer cells
JOURNAL      Patent: US 633152-A 24 25-DEC-2001;
FEATURES     Location/Qualifiers
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                /mol_type="unassigned DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      65 ATGTCCTGTCAG 77
Db      2 ATGTCCTATTAG 14

RESULT 135
AR218751
LOCUS      AR218751              14 bp  DNA          linear    PAT 25-SEP-2002
DEFINITION Sequence 99 from patent US 6420124.
ACCESSION  AR218751
VERSION     AR218751.1  GI:23319646
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
            Connors,T.D., Burn,T.C. and Splawski,I.
TITLE       KVLQ11--a long qt syndrome gene
JOURNAL     Patent: US 6420124-A 99 16-JUL-2002;
            University of Utah Research Foundation and Genzyme Corporation;
            Salt Lake City, UT
FEATURES    Location/Qualifiers
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                /mol_type="genomic DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGT 46
Db      2 TCCTTTAAGAGGT 14

RESULT 136
AR223166
LOCUS      AR223166              14 bp  DNA          linear    PAT 26-SEP-2002
DEFINITION Sequence 99 from patent US 6432644.
ACCESSION  AR223166
VERSION     AR223166.1  GI:23331019
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE       Mutations in the KCNE1 gene encoding human minK which cause
            arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
            Patent: US 6432644-A 99 13-AUG-2002;
            University of Utah Research Foundation; Salt Lake City, UT
FEATURES    Location/Qualifiers
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                /organism="unknown"

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGT 46
Db      2 TCCTTTAAGAGGT 14

RESULT 137
AR229928
LOCUS      AR229928              14 bp  DNA          linear    PAT 20-DEC-2002
DEFINITION Sequence 99 from patent US 6451534.
ACCESSION  AR229928
VERSION     AR229928.1  GI:27269806
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
            Connors,T.D., Burn,T.C. and Splawski,I.
TITLE       KVLQ11--a long QT syndrome gene
JOURNAL     Patent: US 6451534-A 99 17-SEP-2002;
            University of Utah Research Foundation and Genzyme Corporation;
            Salt Lake City, UT
FEATURES    Location/Qualifiers
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                /mol_type="genomic DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGT 46
Db      2 TCCTTTAAGAGGT 14

RESULT 138
AR262184
LOCUS      AR262184              14 bp  DNA          linear    PAT 29-JAN-2003
DEFINITION Sequence 99 from patent US 6323026.
ACCESSION  AR262184
VERSION     AR262184.1  GI:28073545
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE       Mutations in the KCNE1 gene encoding human minK which cause
            arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
            Patent: US 6323026-A 99 27-NOV-2001;
            University of Utah Research Foundation; Salt Lake City, UT
FEATURES    Location/Qualifiers
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Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGT 46
Db      2 TCCTTTAAGAGGT 14

RESULT 139
AR262184
LOCUS      AR262184              14 bp  DNA          linear    PAT 29-JAN-2003
DEFINITION Sequence 99 from patent US 6323026.
ACCESSION  AR262184
VERSION     AR262184.1  GI:28073545
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Keating,M.T., Sanguinetti,M.C. and Splawski,I.
TITLE       Mutations in the KCNE1 gene encoding human minK which cause
            arrhythmia susceptibility thereby establishing KCNE1 as an LQT gene
            Patent: US 6323026-A 99 27-NOV-2001;
            University of Utah Research Foundation; Salt Lake City, UT
FEATURES    Location/Qualifiers
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                /mol_type="genomic DNA"

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      34 TCCTCTGAGAGGT 46
Db      2 TCCTTTAAGAGGT 14

RESULT 139

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AR344622
LOCUS AR344622 14 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 99 from patent US 6582913.
ACCESSION AR344622
VERSION AR344622.1 GI:33740691
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Keating,M.T., Sanguinetti,M.C., Curran,M.E., Landes,G.M.,
Conners,T.D., Burn,T.C. and Splawski,I.
TITLE Diagnostic method for KVLQTL1--a long QT syndrome gene
JOURNAL Patent: US 6582913-A 99 24-JUN-2003;
University of Utah Research Foundation and Genzyme, Inc.; Salt Lake
City, UT
FEATURES
source 1. .14
Location/Qualifiers
/mol_type="genomic DNA"
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14
RESULT 140
AR403429
LOCUS AR403429 14 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1769 from patent US 6623962.
ACCESSION AR403429
VERSION AR403429.1 GI:40150879
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Akhtar,S., Fell,P. and McSwiggen,J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related
to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 1769 23-SEP-2003;
Sirna Therapeutics, Inc. and Aston University; Boulder, CO
FEATURES
source 1. .14
Location/Qualifiers
/mol_type="genomic DNA"
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GACGGCTGGGGA 20
Db 2 GACGGCGGGGCA 14
RESULT 141
AX467015/c
LOCUS AX467015 14 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 44 from Patent WO224950.
ACCESSION AX467015
VERSION AX467015.1 GI:21900356
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Liang,Z., Zhang,H.Y. and Wahlestedt,C.
TITLE Methods and means of rna analysis

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JOURNAL Patent: WO 0224950-A 44 28-MAR-2002;
Neuromics Inc. (US)
FEATURES
source 1. .14
Location/Qualifiers
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetically generated oligonucleotide"
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 61 GCTGATGTCCTCT 73
Db 13 GCTGATGTCCTCT 1
RESULT 142
AX710784/c
LOCUS AX710784 14 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 84 from Patent EP1288296.
ACCESSION AX710784
VERSION AX710784.1 GI:29787165
KEYWORDS
SOURCE Human immunodeficiency virus
ORGANISM Human immunodeficiency virus
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE 1
AUTHORS Draper,K.G., Mcswiggen,J.A., Holecek,J.J., Dudyecz,L.W.,
Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 84 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source 1. .14
Location/Qualifiers
/mol_type="unassigned RNA"
/db_xref="taxon:12721"
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 AAGCTGATGTCCT 71
Db 14 AAGCTGATGTCCT 2
RESULT 143
BD000925/c
LOCUS BD000925 14 bp RNA linear PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD000925
VERSION BD000925.1 GI:18625484
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 14)
AUTHORS Draper,K.G., Dadykztz,L.W., Macswigen,J.A., Maysejak,D.G.,
Holesek,J.J. and Mamone,A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 85 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342285-A/85
PD 12-DEC-2000
PF 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689,14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713,14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823,14-MAY-1992 US 07/882824 PR

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14-MAY-1992 US 07/882886,14-MAY-1992 US 07/882888 PR
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14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKYZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22/(C12N5/10, C12R1:91), PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1:91)
CC
FH Key Location/Qualifiers
FT source 1..14
/organism='Artificial Sequence'.
FEATURES
source
1..14
Location/Qualifiers
/mol_type='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 AAGCTGATGTCCT 71
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DB 14 AAGCTGGTGTCT 2

RESULT 144
BD001354/c
LOCUS
DEFINITION
Method and reagent for inhibiting viral replication.
ACCESSION
BD001354
VERSION
BD001354.1 GI:18625913
KEYWORDS
JP 2000342286-A/85.
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 14)
Draper, K.G., Dadykz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J. and Mamone, A.J.
TITLE
Method and reagent for inhibiting viral replication
JOURNAL
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Artificial Sequence
PN JP 2000342286-A/85
PD 12-DEC-2000
PF 01-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
PR 11-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKYZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE

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PC C12N15/09, C12N5/10, C12N7/00/(A61K38/43, A61K39/125, A61K39/13,
PC A61K39/135,
PC A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
PC A61P1/16,
PC A61P31/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12Q1/68, PC
(C12N15/09, C12R1:93), C12N15/00, C12N5/00, A61K37/48, (C12N15/00, PC
C12R1:93)
CC
FH Key Location/Qualifiers
FT source 1..14
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source
1..14
Location/Qualifiers
/mol_type='synthetic construct'
/mol_type='genomic RNA'
/db_xref='taxon:32630'
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 AAGCTGATGTCCT 71
||||| |||||
DB 14 AAGCTGGTGTCT 2

RESULT 145
S81872811/c
LOCUS
DEFINITION
Gogo-DRB8-MHC-DRB pseudogene [Gorilla gorilla=western lowland
gorilla, ssp. gorilla, Genomic, 14 nt, segment 11 of 12].
ACCESSION
S81875
VERSION
S81875.1 GI:244229
KEYWORDS
.
SEGMENT
11 of 12
SOURCE
Gorilla gorilla (gorilla)
Gorilla gorilla
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Gorilla.
REFERENCE
1 (bases 1 to 14)
Klein, D., Vincek, V., Kasahara, M., Schonbach, C., O'Huigin, C. and
Klein, J.
AUTHORS
Gorilla major histocompatibility complex-DRB pseudogene orthologous
to HLA-DRBVIII
JOURNAL
Hum. Immunol. 32 (3), 211-220 (1991)
PUBMED
1774200
REMARK
GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 81875] from the original journal article.
FEATURES
source
1..14
Location/Qualifiers
/organism='Gorilla gorilla'
/mol_type='genomic DNA'
/db_xref='taxon:9593'
join(S81872.1:6..285,S81873.1:1..111,S81874.1:1..24,1..14)
/genes='Gogo-DRB8'
/notes='MHC-DRB pseudogene'
/pseudo
/codon_start=1
Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 23 CAACTCTGGAGTC 35
||||| |||||
DB 13 CAGCTCAGGAGTC 1

RESULT 146
A57558/c
LOCUS
DEFINITION
Sequence 50 from Patent WO9632483.

```

```

ACCESSION  A57558
VERSION    A57558.1  GI:3713392
KEYWORDS
SOURCE     .
ORGANISM   unidentified
            unclassified
            unclassified sequences.
REFERENCE  1
AUTHORS    Masucci,M.G.
TITLE      IMMUNE-EVADING PROTEINS
JOURNAL    Patent: WO 9632483-A 50 17-OCT-1996;
            MASUCCI MARIA GRAZIA (SE)
COMMENT    Other publication AU 5284296 961030.
FEATURES   Location/Qualifiers
            1..11
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 GGGGATACAC 26
Db 11 GGGGATCCAC 1

RESULT 147
AR030142
LOCUS      AR030142
DEFINITION Sequence 331 from patent US 5861244.
ACCESSION AR030142
VERSION   AR030142.1  GI:5943356
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.

REFERENCE  1 (bases 1 to 11)
AUTHORS    Wang,C.-G. and Hepburn,A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 331 19-JAN-1999;
            Location/Qualifiers
FEATURES   Location/Qualifiers
            1..11
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 40 GAGAGGTAAAG 50
Db 1 GAGAGGGAAG 11

RESULT 148
CQ835708
LOCUS      CQ835708
DEFINITION Sequence 766 from Patent WO2004059001.
ACCESSION CQ835708
VERSION   CQ835708.1  GI:50835242
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 766 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)

QY 54 CAGCGAAGCTG 64
Db 11 CAGCAAGCTG 1

RESULT 150
CQ836081/c
LOCUS      CQ836081/c
DEFINITION Sequence 1139 from Patent WO2004059001.
ACCESSION CQ836081
VERSION   CQ836081.1  GI:50835615
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 1139 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;

FEATURES   Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GGCCTGGGGAT 21
Db 1 GGCCTGGGGGT 11

RESULT 149
CQ835946/c
LOCUS      CQ835946
DEFINITION Sequence 1004 from Patent WO2004059001.
ACCESSION CQ835946
VERSION   CQ835946.1  GI:50835480
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 1004 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTG 64
Db 11 CAGCAAGCTG 1

RESULT 150
CQ836081/c
LOCUS      CQ836081/c
DEFINITION Sequence 1139 from Patent WO2004059001.
ACCESSION CQ836081
VERSION   CQ836081.1  GI:50835615
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 1139 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;

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Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 62 CTGATGTCCTG 72
Db 11 CTGATGTCCTG 1

RESULT 151
LOCUS CQ836100 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1158 from Patent WO2004059001.

ACCESSION CQ836100

VERSION CQ836100.1 GI:50835634

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conrad,M. and Hofmann,K.

TITLE Method for determining markers of human facial skin

JOURNAL Patent: WO 2004059001-A 1158 15-JUL-2004;

Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAAGACGCCT 15
Db 11 CAAGACGCCT 1

RESULT 152
LOCUS CQ837567 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2625 from Patent WO2004059001.

ACCESSION CQ837567

VERSION CQ837567.1 GI:50837101

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conrad,M. and Hofmann,K.

TITLE Method for determining markers of human facial skin

JOURNAL Patent: WO 2004059001-A 2625 15-JUL-2004;

Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
Location/Qualifiers
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGATACACTC 28
Db 1 GGATACACAC 11

RESULT 153
LOCUS CS021382

DEFINITION Sequence 814 from Patent WO2005012576.

ACCESSION CS021382

VERSION CS021382.1 GI:60221937

KEYWORDS synthetic construct

SOURCE synthetic construct
other sequences; artificial sequences.

REFERENCE 1

AUTHORS Sebastian,S.

TITLE Molecular markers for the selection of soybean plants having
superior agronomic performance

JOURNAL Patent: WO 2005012576-A 814 10-FEB-2005;
Pioneer Hi-Bred International Inc. (US)

FEATURES
source
1. .11
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide probe"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 49 AGAGCCAGCGA 59
Db 1 AGAGCCAGTGA 11

RESULT 154
LOCUS CS058360

DEFINITION Sequence 257 from Patent WO2005028671.

ACCESSION CS058360

VERSION CS058360.1 GI:62551543

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.

TITLE Method for determining hair cycle markers

JOURNAL Patent: WO 2005028671-A 257 31-MAR-2005;

Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 48 AAGAGCCAGCG 58
Db 1 AAGAGCCAGCG 11

RESULT 155
LOCUS CS058436

DEFINITION Sequence 333 from Patent WO2005028671.

ACCESSION CS058436

VERSION CS058436.1 GI:62551619

KEYWORDS

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SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
TITLE       Method for determining hair cycle markers
JOURNAL     Patent: WO 2005028671-A 333 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  48 AAGAGCCAGCG 58
    |||||
Db  1 AAGAACCAGCG 11

RESULT 156
LOCUS      CS058451                11 bp      DNA      linear      PAT 13-APR-2005
DEFINITION Sequence 348 from Patent WO2005028671.
ACCESSION  CS058451
VERSION     CS058451.1 GI:62551634
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
TITLE       Method for determining hair cycle markers
JOURNAL     Patent: WO 2005028671-A 348 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  11 GGCCTGGGGAT 21
    |||||
Db  1 GGCCTGGGGAT 11

RESULT 157
LOCUS      CS058533                11 bp      DNA      linear      PAT 13-APR-2005
DEFINITION Sequence 430 from Patent WO2005028671.
ACCESSION  CS058533
VERSION     CS058533.1 GI:62551716
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and

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Kessler-Becker,D.
Method for determining hair cycle markers
Patent: WO 2005028671-A 430 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  40 GACAGGTAAAG 50
    |||||
Db  1 GACAGGTAAAG 11

RESULT 158
LOCUS      AX625866/c                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2907 from Patent WO02053774.
ACCESSION  AX625866
VERSION     AX625866.1 GI:28453904
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2907 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 88;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  54 CACGAGAGCTG 64
    |||||
Db  11 CACGAGAGCTG 1

RESULT 159
LOCUS      AX627490                11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4531 from Patent WO02053774.
ACCESSION  AX627490
VERSION     AX627490.1 GI:28455528
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4531 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

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Query Match 12.2%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 88;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GGCCTGGGGAT 21
 |||||
 Db 1 GGCCTGGGGGT 11

RESULT 160
 AX628152 11 bp DNA linear PAT 21-FEB-2003
 LOCUS
 DEFINITION Sequence 5193 from Patent WO02053774.
 ACCESSION AX628152
 VERSION AX628152.1 GI:28456190
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1
 AUTHORS Petersohn, D., Conradt, M. and Hofmann, K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 5193 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
 source 1..11
 Location/Qualifiers
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 88;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 GGATACAACTC 28
 |||||
 Db 1 GGATACAAACAC 11

RESULT 161
 AX630121 11 bp DNA linear PAT 21-FEB-2003
 LOCUS
 DEFINITION Sequence 7162 from Patent WO02053774.
 ACCESSION AX630121
 VERSION AX630121.1 GI:28458159
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1
 AUTHORS Petersohn, D., Conradt, M. and Hofmann, K.
 TITLE Method for determining homeostasis of the skin
 JOURNAL Patent: WO 02053774-A 7162 11-JUL-2002;
 Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
 source 1..11
 Location/Qualifiers
 1..11
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 12.2%; Score 9.4; DB 1; Length 11;
 Best Local Similarity 90.9%; Pred. No. 88;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 56 GCGAAGCTGAT 66
 |||||
 Db 1 GTGAAGCTGAT 11

RESULT 162
 BD240909/c

LOCUS
 DEFINITION Expression and export of angiogenesis inhibitors as immunofusins.
 ACCESSION BD240909
 VERSION BD240909.1 GI:33050679
 KEYWORDS JP 2002523036-A/29.
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 12)
 AUTHORS Lo, K.M., Li, Y. and Gillies, S.D.
 TITLE Expression and export of angiogenesis inhibitors as immunofusins
 JOURNAL Patent: JP 2002523036-A 29 30-JUL-2002;
 LEXIGEN PHARMACEUTICALS CORP

COMMENT OS Artificial Sequence
 PN JP 2002523036-A/29
 PD 30-JUL-2002
 PF 25-AUG-1999 JP 2000566305
 PR 25-AUG-1998 US 60/097883
 PI KIN MING LO, YUE LI, STEPHEN D GILLIES
 PC C12N15/09, A61K31/711, A61K38/00, A61K39/395, A61K48/00, A61P7/00,
 PC A61P35/00,
 PC A61P43/00, C07K14/745, C07K19/00, C12N5/10, C12P21/02,
 PC C12N15/00,
 PC C12N5/00, A61K37/02
 CC Description of Artificial Sequence: BamHI/HindIII CC linker:
 top strand
 FH Key Location/Qualifiers
 FT CDS (3)..(11).

FEATURES
 source 1..12
 Location/Qualifiers
 1..12
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 93;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GGCCTGGGGAT 21
 |||||
 Db 12 GGCCTGAGGAT 2

RESULT 163
 CQ766172/c

LOCUS
 DEFINITION Sequence 133 from Patent WO2004005547.
 ACCESSION CQ766172
 VERSION CQ766172.1 GI:44908432
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Weinzierl, R.
 TITLE Method
 JOURNAL Patent: WO 2004005547-A 133 15-JAN-2004;
 IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)

FEATURES
 source 1..12
 Location/Qualifiers
 1..12
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="HS consensus sequence"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 93;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 62 CTGATGCTCTG 72

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Db      11 CAGATGCTCTG 1
      | | | | | | | | | |
RESULT 164
LOCUS   CQ766282/c
DEFINITION Sequence 243 from Patent WO2004005547.
ACCESSION CQ766282
VERSION   CQ766282.1 GI:44908542
KEYWORDS .
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Weinzierl, R.
TITLE    Patent: WO 2004005547-A 243 15-JAN-2004;
JOURNAL  IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES
source   1. .12
         /organism="synthetic construct"
         /mol_type="unassigned DNA"
         /db_xref="taxon:32630"
         /note="HS motif"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      58 GAAGCTGATGT 68
Db      12 GAAGCTGTTGT 2

RESULT 165
LOCUS   CS104143
DEFINITION Sequence 8 from Patent WO2005049808.
ACCESSION CS104143
VERSION   CS104143.1 GI:67512417
KEYWORDS .
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Hashiguchi, K., Nakai, Y. and Itou, H.
TITLE    Method for producing l-amino acid by fermentation
JOURNAL  Patent: WO 2005049808-A 8 02-JUN-2005;
JOURNAL  Ajinomoto Co., Inc. (JP)
FEATURES
source   1. .12
         /organism="synthetic construct"
         /mol_type="unassigned DNA"
         /db_xref="taxon:32630"
         /note="Description of Artificial Sequence : XbaI linker
         for linkage to thrA and a ttenuator"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTC 35
Db      2 ACTCTAGAGTC 12

RESULT 166
LOCUS   CS104143/c
DEFINITION Sequence 8 from Patent WO2005049808.
ACCESSION CS104143
VERSION   CS104143.1 GI:67512417

```

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KEYWORDS .
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Hashiguchi, K., Nakai, Y. and Itou, H.
TITLE    Method for producing l-amino acid by fermentation
JOURNAL  Patent: WO 2005049808-A 8 02-JUN-2005;
JOURNAL  Ajinomoto Co., Inc. (JP)
FEATURES
source   1. .12
         /organism="synthetic construct"
         /mol_type="unassigned DNA"
         /db_xref="taxon:32630"
         /note="Description of Artificial Sequence : XbaI linker
         for linkage to thrA and a ttenuator"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      25 ACTCTGGAGTC 35
Db      11 ACTCTAGAGTC 1

RESULT 167
LOCUS   AR475028
DEFINITION Sequence 415 from patent US 6692917.
ACCESSION AR475028
VERSION   AR475028.1 GI:42714165
KEYWORDS .
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 12)
AUTHORS  Neri, B. P., Hall, J. G., Lyamichiev, V. and Smith, L. M.
TITLE    Systems and methods for invasive cleavage reaction on dendrimers
JOURNAL  Patent: US 6692917-A 415 17-FEB-2004;
JOURNAL  Third Wave Technologies, INC; Madison, WI
FEATURES
source   1. .12
         /organism="unknown"
         /mol_type="genomic DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      31 GAGTCCTCTGA 41
Db      1 GAGTCCTCTGA 11

RESULT 168
LOCUS   AX097978
DEFINITION Sequence 46 from Patent WO0118048.
ACCESSION AX097978
VERSION   AX097978.1 GI:13514757
KEYWORDS .
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  van Eijs, G. J., Hateboer, G. and Havenga, M. J.
TITLE    Smooth muscle cell promoter and uses thereof
JOURNAL  Patent: WO 0118048-A 46 15-MAR-2001;
JOURNAL  Introgene B.V. (NL)
FEATURES
source   1. .12
         /organism="synthetic construct"

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="variant intron-exon splice recognition sequences"

Query Match      12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 40 GAGAGGTTAAAG 50
|||||
Db 2 GAGAGGTTAGAG 12

RESULT 169
LOCUS AX138554 12 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 46 from Patent EP1083231.
ACCESSION AX138554
VERSION AX138554.1 GI:14274449
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Smooth muscle cell promoter and uses thereof
TITLE Patent: EP 1083231-A 46 14-MAR-2001;
JOURNAL Introgene B.V. (NL)
FEATURES
source
1. .12
Location/Qualifiers
/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="variant intron-exon splice recognition sequences"

Query Match      12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 40 GAGAGGTTAAAG 50
|||||
Db 2 GAGAGGTTAGAG 12

RESULT 170
LOCUS AX772212/c 12 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 2 from Patent WO03042407.
ACCESSION AX772212
VERSION AX772212.1 GI:32438785
KEYWORDS
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
AUTHORS Rukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
TITLE Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
JOURNAL Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1
AUTHORS Dickson, B., Berger, J., Suzuki, T. and Knoblich, J.
TITLE Method for identifying therapeutic targets by use of genetic
screens in drosophila melanogaster
JOURNAL Patent: WO 03042407-A 2 22-MAY-2003;
BOHRINGER INGELHEIM INTERNATIONAL GMBH; CD Patents (DE)
FEATURES
source
1. .12
Location/Qualifiers
/mol_type="Drosophila melanogaster"
/mol_type="unassigned DNA"
/db_xref="taxon:7227"

Query Match      12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 93;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 62 CTGATGTCCTG 72

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="variant intron-exon splice recognition sequences"

Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAA 60
|||||
Db 3 GAGCCAGCTAA 13

RESULT 171
LOCUS AR019451 13 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 39 from patent US 5783431.
ACCESSION AR019451
VERSION AR019451.1 GI:3974565
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Peterson, T.C., Foster, L.M. and Brian, P.
TITLE Methode for generating and screening novel metabolic pathways
JOURNAL Patent: US 5783431-A 39 21-JUL-1998;
FEATURES
source
1. .13
Location/Qualifiers
/mol_type="unassigned DNA"

Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAA 60
|||||
Db 3 GAGCCAGCTAA 13

RESULT 172
LOCUS AR029150/c 13 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 26 from patent US 5859221.
ACCESSION AR029150
VERSION AR029150.1 GI:5941123
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Cook, P. Dan. and Kawasaki, A. Mamoru.
TITLE 2'-modified oligonucleotides
JOURNAL Patent: US 5859221-A 26 12-JAN-1999;
FEATURES
source
1. .13
Location/Qualifiers
/mol_type="unassigned DNA"

Query Match      12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGG 17
|||||
Db 12 AAACGGCCTGG 2

RESULT 173
LOCUS AR036534/c 13 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 26 from patent US 5972232.
ACCESSION AR036534
VERSION AR036534.1 GI:5953202
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Cook, P. Dan. and Kawasaki, A. Mamoru.
TITLE 2'-O-modified oligonucleotides
```

JOURNAL Patent: US 5872232-A 26 16-FEB-1999;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17
| | | | | | | | | |
Db 12 AACGGCCTGG 2

RESULT 174
LOCUS AR096067/c 13 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 26 from patent US 6005087.
ACCESSION AR096067
VERSION AR096067.1 GI:10024532
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Cook, P. Dan. and Kawasaki, A. Mamoru.
TITLE 2'-modified oligonucleotides
JOURNAL Patent: US 6005087-A 26 21-DEC-1999;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17
| | | | | | | | | |
Db 12 AACGGCCTGG 2

RESULT 175
LOCUS AR156401 13 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 30 from patent US 6242211.
ACCESSION AR156401
VERSION AR156401.1 GI:15125105
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Peterson, T. C. and Brian, P.
TITLE Methods for generating and screening novel metabolic pathways
JOURNAL Patent: US 6242211-A 30 05-JUN-2001;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAA 60
| | | | | | | | | |
Db 3 GAGCCAGCTAA 13

RESULT 176
LOCUS AR174824/c 13 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 26 from patent US 639754.
ACCESSION AR212300
VERSION AR212300.1 GI:21515837
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Cook, P. Dan.
TITLE Sugar modified oligonucleotides

JOURNAL Patent: US 6307040-A 6 23-OCT-2001;
FEATURES Location/Qualifiers
source 1..13
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17
| | | | | | | | | |
Db 12 AACGGCCTGG 2

RESULT 177
LOCUS CQ828552 13 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 270 from Patent WO2004053120.
ACCESSION CQ828552
VERSION CQ828552.1 GI:49732035
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1
AUTHORS Weihe, E., Bieller, A. and Schaefer, M. K.
TITLE Regulatory elements in the 5' region of the vrl gene
JOURNAL Patent: WO 2004053120-A 270 24-JUN-2004;
FEATURES Location/Qualifiers
source 1..13
/organism="Rattus norvegicus"
/mol_type="unassigned DNA"
/db_xref="taxon:10116"
/note="V\$GATA1 04"

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 98;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 62 CTGATGTCCTG 72
| | | | | | | | | |
Db 3 CTGATATCTG 13

RESULT 178
LOCUS AR212300/c 13 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 26 from patent US 639754.
ACCESSION AR212300
VERSION AR212300.1 GI:21515837
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13)
AUTHORS Cook, P. Dan.
TITLE Sugar modified oligonucleotides

JOURNAL	Patent: US 6399754-A 26 04-JUN-2002;	LOCUS	13 bp	RNA	linear	PAT 10-APR-2003
FEATURES	Location/Qualifiers	1. .13				
source	/organism="unknown"					
	/mol_type="unassigned DNA"					
Query Match	12.2%; Score 9.4; DB 1; Length 13;					
Best Local Similarity	90.9%; Pred. No. 98;					
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	7 AGACGGCGCTGG 17					
DB	12 AAACGGCGCTGG 2					
RESULT 179						
LOCUS	AR285769	13 bp	RNA	linear		PAT 10-APR-2003
DEFINITION	Sequence 141 from patent US 6528640.					
ACCESSION	AR285769					
VERSION	AR285769.1 GI:29723363					
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 13)					
AUTHORS	Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,					
TITLE	Matulic-Adamic,J., Sweedler,D. and Zinnen,S.					
JOURNAL	Synthetic ribonucleic acids with RNase activity					
Patent:	US 6528640-A 141 04-MAR-2003;					
FEATURES	Ribozyme Pharmaceuticals, incorporated; Boulder, CO					
source	Location/Qualifiers					
	1. .13					
	/organism="unknown"					
	/mol_type="unassigned RNA"					
Query Match	12.2%; Score 9.4; DB 1; Length 13;					
Best Local Similarity	90.9%; Pred. No. 98;					
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	47 AAAGAGCCAGC 57					
DB	2 AGAGAGCCAGC 12					
RESULT 180						
LOCUS	AR397760	13 bp	RNA	linear		PAT 18-DEC-2003
DEFINITION	Sequence 141 from patent US 6617438.					
ACCESSION	AR397760					
VERSION	AR397760.1 GI:40135004					
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 13)					
AUTHORS	Beigelman,L., Burgin,A.B., Beaudry,A., Karpeisky,A.,					
TITLE	Matulic-Adamic,J., Sweedler,D. and Zinnen,S.					
JOURNAL	Oligoribonucleotides with enzymatic activity					
Patent:	US 6617438-A 141 09-SEP-2003;					
FEATURES	Sirna Therapeutics, Inc.; Boulder, CO					
source	Location/Qualifiers					
	1. .13					
	/organism="unknown"					
	/mol_type="unassigned RNA"					
Query Match	12.2%; Score 9.4; DB 1; Length 13;					
Best Local Similarity	90.9%; Pred. No. 98;					
Matches	10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	47 AAAGAGCCAGC 57					
DB	2 AGAGAGCCAGC 12					

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 16:04:57 ; Search time 0.001 Seconds
 (without alignments)
 12.936 Million cell updates/sec

Title: US-10-643-038-17_994-1070
 Perfect score: 77
 Sequence: 1 caacaagagcgctgggga.....gaagctgatctctgtcaag 77

Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 84 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 8 summaries

Database : estdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Length	DB ID	Description	SUMMARIES
C 1	9	11.7	11 1	AJ651054	ACCESSION:AJ651054
C 2	8.4	10.9	11 1	AJ590125	ACCESSION:AJ590125
C 3	8.4	10.9	11 1	CL981148	ACCESSION:CL981148
4	7.8	10.1	11 1	BQ111753	ACCESSION:BQ111753
5	7.4	9.6	10 1	BQ789997	ACCESSION:BQ789997
6	7.4	9.6	10 1	CL659790	ACCESSION:CL659790
7	7.4	9.6	10 1	CL686823	ACCESSION:CL686823
8	7.4	9.6	10 1	T7115122	ACCESSION:CT007455

ALIGNMENTS

RESULT 1
 AJ651054/c
 LOCUS
 DEFINITION AJ651054 CSEQRAN19 Sus scrofa cDNA clone C0003277_B19, mRNA
 11 bp mRNA linear EST 07-JUL-2004

ACCESSION AJ651054
 VERSION AJ651054.1 GI:49327899
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 11)
 Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
 TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 JOURNAL Unpublished (2004)
 COMMENT Contact: Anderson SI
 Genomics and Bioinformatics

Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13f Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.

FEATURES source

1. .11
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /clone="C0003277_B19"
 /tissue_type="ovary"
 /clone_lib="CSEQRAN19"
 /notes="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing; Normalised library constructed from pooled ovaries"

Query Match 11.7%; Score 9; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4 ACAAGACGG 12
 |||||
 Db 9 ACAAGACGG 1

RESULT 2

AJ590125/c

LOCUS

DEFINITION AJ590125 11 bp DNA linear GSS 15-JAN-2004

Arabidopsis thaliana T-DNA flanking sequence, left border, clone

563G02, genomic survey sequence.

ACCESSION AJ590125 GI:37939749

VERSION

KEYWORDS GSS; left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1

AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,

Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,

Lepiniec,L., Caboche,M. and Lecharny,A.

T-DNA integration into the Arabidopsis genome depends on sequences

of pre-insertion sites

EMBO Rep. 3 (12), 1152-1157 (2002)

PUBMED 12446565

REFERENCE 2 (bases 1 to 11)

AUTHORS Balzergue,S.

TITLE Direct Submission

JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE

PCR was performed on DNA from transformants of Arabidopsis thaliana

plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border

to determine the genomic sequence flanking the insertion. T-DNA

derived sequences were removed. Information to order the

corresponding mutant line and a link to a database providing a

graphical display of the insertion site are available at

http://dbsgap.versailles.inra.fr/publiclines/. This sequence has

been generated in the framework of the French plant genomics

program 'Genoplante' (http://www.genoplante.com and

http://genoplante-info.inbio.gen.fr).

FEATURES source

1. .11

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="563G02"

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/misc_feature      /clone lib="Arabidopsis thaliana T-DNA insertion lines"
                  1. .11
/notes="T-DNA flanking sequence
left border"

Query Match      10.9%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 42 GAGTAAGA 51
Db 11 GAGTAAGAAA 2

RESULT 3
CL983148/c
LOCUS
DEFINITION      GC0387 TIGEM gene trap library Mus musculus cDNA clone A012.B10,
mRNA sequence.
ACCESSION      CL983148
VERSION        CL983148.1 GI:52420779
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Cobellis,G., Nicolaus,G., Iovino,M., Romito,A., Marra,E.,
Ballabio,A., Sardiello,M., Di Giorgio,P.P., Iovino,N., Zollo,M.,
Barbaisio,A. and Cortese,R.
TITLE          Tagging genes with cassette-exchange sites
JOURNAL        Nucleic Acids Res. 33 (4), e44 (2005)
PUBMED        15741177
COMMENT        Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene Trap.
FEATURES
source
1. .11
Location/Qualifiers
/mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Cobellis,G., Nicolaus,G., Iovino,M., Romito,A., Marra,E.,
Ballabio,A., Sardiello,M., Di Giorgio,P.P., Iovino,N., Zollo,M.,
Barbaisio,A. and Cortese,R.
TITLE          Tagging genes with cassette-exchange sites
JOURNAL        Nucleic Acids Res. 33 (4), e44 (2005)
PUBMED        15741177
COMMENT        Contact: TIGEM
107
TIGEM
Via P. Castellino, 111, 80131 NAPOLI, ITALY
Tel: +390816132205
Fax: +390815790919
Email: cobellis@tigem.it
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from TIGEM. Annotation information
available from TIGEM
Class: Gene Trap.

/misc_feature      /clone lib="Arabidopsis thaliana T-DNA insertion lines"
                  1. .11
/notes="T-DNA flanking sequence
left border"

Query Match      10.9%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCT 37
Db 11 CTGGGGTCCT 2

RESULT 4
BQ111753
LOCUS
DEFINITION      EST597329 mixed potato tissues Solanum tuberosum cDNA clone STMCC84
5' end, mRNA sequence.
BQ111753
1 GI:20163715
EST.
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiids; Solanales; Solanaceae; Solanum.
REFERENCE      1 (bases 1 to 11)
AUTHORS        Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
Karamycheva,S.A.
TITLE          Generation of a set of potato cDNA clones for microarray analyses
JOURNAL        Unpublished (2002)
COMMENT        Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: T3.
FEATURES
source
1. .11
Location/Qualifiers
/organism="Solanum tuberosum"
/mol type="mRNA"
/cultivar="Kennebec or Binjite"
/db_xref="taxon:4113"
/cloned="STMCC84"
/tissue_type="mixed tissues"
/lab host="SOLR"
/clone lib="mixed potato tissues"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."

Query Match      10.1%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 45 GTAAAGAGCCA 55
Db 1 GGAAGAGCCA 11

RESULT 5
BQ789997
LOCUS
DEFINITION      BQ789997 10 bp mRNA linear EST 30-JUL-2002
hage005AD02 Heterobasidion annosum - Scots pine infection stage
(HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion
annosum mixed EST library cDNA clone hage005AD02, mRNA sequence.
BQ789997
1 GI:22004959
EST.
Pinus sylvestris/Heterobasidion annosum mixed EST library
Pinus sylvestris/Heterobasidion annosum mixed EST library
Rukaryota; mixed EST libraries.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Asiegbu,F.O., Nahalkova,J. and Dean,R.A.
TITLE          Selected Expressed sequence tags of cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
seedling roots of Scots pine (Pinus sylvestris)
JOURNAL        Unpublished (2001)
COMMENT        Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
Sweden
Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se

```



```

FEATURES
  source
    Seq primer: T7 primer.
    Location/Qualifiers
      1..10
        EST library="Pinus sylvestris/Heterobasidion annosum mixed
        /mol_type="mRNA"
        /db_xref="taxon:169015"
        /clone="hege005ab02"
        /dev_stage="Seedling roots of scots pine were infected for
        6 days with H. annosum"
        /clone_lib="Heterobasidion cDNA library"
        /note="vector: pT-Adv; Site 1: EcoRI; The subtractive
        hybridization cDNA library was constructed from scots pine
        roots infected for 6-days with mycelia of Heterobasidion
        annosum (FP5)."
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Query Match 9.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 CTCTGAGAG 44
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 Db 1 CTCTGATAG 9

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RESULT 6
LOCUS
  CL659790
  DEFINITION
    CL659790 B11 - PRI0135b.B21 (10) Mixed stage fosmid library of P.
    pacificus var. California Pristionchus pacificus genomic, genomic
    survey sequence.
  ACCESSION
    CL659790
  VERSION
    CL659790.1 GI:50144248
  KEYWORDS
    GSS.
  SOURCE
    Pristionchus pacificus
    Pristionchus pacificus
    Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
    Neodiplogasteridae; Pristionchus.
  REFERENCE
    1 (bases 1 to 10)
    Srinivasan,J., Otto,G.W., Kahlou,U., Geisler,R. and Sommer,R.J.
    AppADB: an Acedb database for the nematode satellite organism
  AUTHORS
    Srinivasan,J., Otto,G.W., Kahlou,U., Geisler,R. and Sommer,R.J.
  TITLE
    This library was generated at Caltech, Pasadena, USA and end
    sequenced at Vancouver, Canada.
  JOURNAL
    Nucleic Acids Res. 32 (1), D421-D422 (2004)
  PUBMED
    14681447
  COMMENT
    Contact: Sommer RJ
    Evolutionary Biology
    Max-Planck-Institute for Developmental Biology
    Spemannstr. 37-39, Tuebingen D-72076, Germany
    Tel: 00497071601371
    Fax: 00497071601498
    Email: ralf.sommer@tuebingen.mpg.de
    This library was generated at Caltech, Pasadena, USA and end
    sequenced at Vancouver, Canada.
    Seq primer: T7
    Class: fosmid ends.
    Location/Qualifiers
      1..10
        /organism="Pristionchus pacificus"
        /mol_type="genomic DNA"
        /strain="California"
        /db_xref="taxon:54126"
        /clone_lib="Mixed stage fosmid library of P. pacificus
        var. California"
        /note="Vector: pBpifos-5 Fosmid vector"
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Query Match 9.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 44 GGTAAAGAG 52
 |||||
 Db 10 GATAAAGAG 2

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RESULT 8
LOCUS
  T7115122
  DEFINITION
    T7115122 Equus caballus GSS, BAC clone CH241-115122, T7 end sequence,
    genomic survey sequence.
  ACCESSION
    CT007455
  VERSION
    CT007455.1 GI:67967256
  KEYWORDS
    GSS; genomic survey sequence.
  SOURCE
    Equus caballus (horse)
    Equus caballus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
  REFERENCE
    1 (bases 1 to 10)
    Leeb,T., Binns,M.M., de Jong,P.J., Berg,C., Conrad,A., Jarek,M.,
    Loehmert,T.H., Nordstiek,G., Severitt,S., Scharfe,S.,
    Schindewolf,C., Schrader,F., Thies,S. and Bloecker,H.
    Analysis of horse BAC sequences
  AUTHORS
    Unpublished
    2 (bases 1 to 10)
    Jarek,M.
  TITLE
    Direct Submission
  JOURNAL
    Submitted (10-JUN-2005) of Genome Analysis, German Research Centre
```

```

RESULT 7
LOCUS
  CL686823/c
  DEFINITION
    CL686823 A03.2 - PRI0145b.BR (10) Mixed stage fosmid library of P.
    pacificus var. California Pristionchus pacificus genomic, genomic
    survey sequence.
  ACCESSION
    CL686823
  VERSION
    CL686823.1 GI:50195421
  KEYWORDS
    GSS.
  SOURCE
    Pristionchus pacificus
    Pristionchus pacificus
    Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
    Neodiplogasteridae; Pristionchus.
  REFERENCE
    1 (bases 1 to 10)
    Srinivasan,J., Otto,G.W., Kahlou,U., Geisler,R. and Sommer,R.J.
    AppADB: an Acedb database for the nematode satellite organism
  AUTHORS
    Srinivasan,J., Otto,G.W., Kahlou,U., Geisler,R. and Sommer,R.J.
  TITLE
    This library was generated at Caltech, Pasadena, USA and end
    sequenced at Vancouver, Canada.
  JOURNAL
    Nucleic Acids Res. 32 (1), D421-D422 (2004)
  PUBMED
    14681447
  COMMENT
    Contact: Sommer RJ
    Evolutionary Biology
    Max-Planck-Institute for Developmental Biology
    Spemannstr. 37-39, Tuebingen D-72076, Germany
    Tel: 00497071601371
    Fax: 00497071601498
    Email: ralf.sommer@tuebingen.mpg.de
    This library was generated at Caltech, Pasadena, USA and end
    sequenced at Vancouver, Canada.
    Seq primer: T7
    Class: fosmid ends.
    Location/Qualifiers
      1..10
        /organism="Pristionchus pacificus"
        /mol_type="genomic DNA"
        /strain="California"
        /db_xref="taxon:54126"
        /clone_lib="Mixed stage fosmid library of P. pacificus
        var. California"
        /note="Vector: pBpifos-5 Fosmid vector"
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Query Match 9.6%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 3.8;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 44 GGTAAAGAG 52
 |||||
 Db 10 GATAAAGAG 2

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RESULT 8
LOCUS
  T7115122
  DEFINITION
    T7115122 Equus caballus GSS, BAC clone CH241-115122, T7 end sequence,
    genomic survey sequence.
  ACCESSION
    CT007455
  VERSION
    CT007455.1 GI:67967256
  KEYWORDS
    GSS; genomic survey sequence.
  SOURCE
    Equus caballus (horse)
    Equus caballus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
  REFERENCE
    1 (bases 1 to 10)
    Leeb,T., Binns,M.M., de Jong,P.J., Berg,C., Conrad,A., Jarek,M.,
    Loehmert,T.H., Nordstiek,G., Severitt,S., Scharfe,S.,
    Schindewolf,C., Schrader,F., Thies,S. and Bloecker,H.
    Analysis of horse BAC sequences
  AUTHORS
    Unpublished
    2 (bases 1 to 10)
    Jarek,M.
  TITLE
    Direct Submission
  JOURNAL
    Submitted (10-JUN-2005) of Genome Analysis, German Research Centre
```

for Biotechnology, Mascheroder Weg 1, Braunschweig D-38124, Germany

FEATURES

source

Location/Qualifiers

1..10

/organism="Equus caballus"

/mol_type="genomic DNA"

/db_xref="taxon:9796"

/clone="CH241-115122"

/clone_lib="CHORI-241"

/note="sequenced with T7 primer"

Query Match

Best Local Similarity 9.6%; Score 7.4; DB 1; Length 10;

Matches 8; Conservativity 88.9%; Pred.No.3.8;

Mismatches 0; Indels 1; Gaps 0;

Qy 20 ATCAACTC 28

|||||

Db 2 ATAGGACTC 10

Search completed: April 19, 2006, 16:04:57

Job time : 0.001 secs

XX This oligonucleotide can hybridize to nucleic acids encoding
 CC phospholipase A2 typical of the synovial fluid of patients with
 CC rheumatoid arthritis. (SF-PLA2 is more closely related to group II PLA2
 CC enzymes such as those in rattlesnake venom than to pancreatic PLA2). The
 CC oligonucleotide (especially its phosphorothioate analogue) would be
 CC useful in inhibiting SF-PLA2 expression. SF-PLA2 secretion has been
 CC detected from a human epidermal carcinoma cell line and primary human
 CC epidermal keratinocytes. This suggests that the inhibitory
 CC oligonucleotide would be useful in the treatment of inflammatory
 CC disorders of the skin. See AAQ14859-Q14895
 XX
 SQ Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 27.3%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATACAACTCTGGAGTCTCTG 40
 |||||
 Db 21 ATACAACTCTGGAGTCTCTG 1

RESULT 3
 AAQ61918/c
 ID AAQ61918 standard; DNA; 21 BP.
 XX
 AC AAQ61918;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX
 DE Human type II phospholipase A2 inhibiting oligomer, ISIS no 3182.

XX
 KW Inhibition; replication; herpes simplex virus; HSV; HIV; aging;
 KW human cytomegalovirus; influenza virus; inflammation; telomere length;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT misc_feature 1..21
 FT /*tag= a
 FT /note= "Phosphorothioate intersugar linkages"

XX WO9408053-A1.
 XX
 PD 14-APR-1994.
 XX
 PF 29-SEP-1993; 93WO-US009297.
 XX
 PR 29-SEP-1992; 92US-00954185.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
 PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
 XX
 DR WPI; 1994-135613/16.

XX
 PT New modified oligo-nucleotide contg guanine quartet - inhibits activity
 PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 PT of chromosomes.

XX
 PS Disclosure; Page 26; 144pp; English.

XX The sequences given in AAQ61917-55 are oligonucleotides which contain a
 CC G4 stretch and which may be used for inhibiting phospholipase A2 enzyme
 CC activity. Oligonucleotides such as these may also be used for inhibiting
 CC activity of HSV, HIV, human cytomegalovirus or influenza virus, or for
 CC treating inflammatory and neurological disorders caused by phospholipase
 CC A2 activity in cases of hyperproliferation, malignancy, cardiovascular

CC disease and snake bite. They may also be used for inhibiting division of
 CC malignant cells by modulating telomere length, which may also retard
 CC aging. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 21 BP; 6 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 27.3%; Score 21; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.9;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATACAACTCTGGAGTCTCTG 40
 |||||
 Db 21 ATACAACTCTGGAGTCTCTG 1

RESULT 4
 ACC46928/c
 ID ACC46928 standard; DNA; 20 BP.

XX
 AC ACC46928;

XX
 DT 05-JUN-2003 (first entry)

XX Human phospholipase A2 antisense oligonucleotide SEQ ID NO:25.

XX
 KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
 KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
 KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
 KW psoriasis; diabetes; ss.

XX Homo sapiens.
 OS Synthetic.

Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"

XX WO200297133-A1.

XX
 PD 05-DEC-2002.

XX
 PF 21-MAY-2002; 2002WO-US016135.

XX
 PR 25-MAY-2001; 2001US-00865866.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

XX WPI; 2003-140495/13.

XX New compound that hybridizes with and inhibits the expression of
 PT phospholipase A2, group IIA, useful for preparing a composition for
 PT treating or preventing inflammation, cancer, psoriasis or diabetes.

XX Claim 3; Page 86; 135pp; English.

XX The present invention describes a compound (I) comprising 8-50
 CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
 CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
 CC A2, group IIA (synovial), where the compound specifically hybridizes with
 CC and inhibits the expression of phospholipase A2, group IIA (synovial).
 CC Also described: (1) a composition comprising the compound and a carrier

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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 16:12:08 ; Search time 0.001 Seconds
(without alignments)
677.446 Million cell updates/sec

Title: US-10-643-038-17_994-1070

Perfect score: 77

Sequence: 1 caacaagacggctgggga.....gaagctgatgtctgtctaag 77

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 292 seqs, 4399 residues

Total number of hits satisfying chosen parameters: 584

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 299 summaries

Database : ngsdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	28.2	36.6	33	1	AAQ26374
C 2	21	27.3	21	1	AAQ14886
C 3	21	27.3	21	1	AAQ61918
C 4	20	26.0	20	1	ACC46928
C 5	20	26.0	20	1	ACC46927
C 6	20	26.0	20	1	ACC46926
C 7	20	26.0	20	1	ACC46925
C 8	20	26.0	20	1	ACC46922
C 9	20	26.0	20	1	ACC46924
C 10	20	26.0	20	1	ACC46923
C 11	17.8	23.1	21	1	ACL45000
C 12	16.8	21.8	21	1	ACL44998
C 13	16.8	21.8	21	1	ACL44994
C 14	16.8	21.8	21	1	ACL44996
C 15	16.4	21.3	21	1	ACL44495
C 16	16.4	21.3	21	1	ACL44497
C 17	16.4	21.3	21	1	ACL44499
C 18	16.4	21.3	21	1	ACL44999
C 19	16	20.8	20	1	AA748824
C 20	15.8	20.5	21	1	ADZ97584
C 21	15.4	20.0	21	1	ACL44498
C 22	15.4	20.0	22	1	ADD35279
C 23	15.2	19.7	20	1	ADK72854
C 24	15.2	19.7	20	1	ADK72874
C 25	14.8	19.2	20	1	ABL44489
C 26	14.8	19.2	21	1	AAD35822
C 27	14.8	19.2	21	1	ADT92489
C 28	14.8	19.2	21	1	ADS93548
C 29	14.8	19.2	21	1	ACL44492
C 30	14.4	18.7	17	1	ABN10034
C 31	14.4	18.7	17	1	ABN10035
C 32	14.4	18.7	17	1	ACN73125
C 33	14.4	18.7	17	1	ACN73124

C 34	14.4	18.7	18	1	AAZ31818	Human G-alpha-13 a
C 35	14.2	18.4	20	1	ADK74660	Chimeric phosphoro
C 36	14.2	18.4	20	1	ADK73231	Chimeric phosphoro
C 37	14.2	18.4	20	1	ADP12043	Set 2 right PCR pr
C 38	14	18.2	17	1	ABN10033	Human GDMPL-1 17-m
C 39	14	18.2	17	1	ABN10032	Human GDMPL-1 17-m
C 40	14	18.2	17	1	ACN73122	Human GDMPL-1 prob
C 41	14	18.2	17	1	ACN73123	Human GDMPL-1 prob
C 42	13.8	17.9	17	1	ADK04443	Human Na/H exchang
C 43	13.4	17.4	15	1	ADJ82395	KLMSY-encoding nuc
C 44	13.4	17.4	17	1	ABN10036	Human GDMPL-1 17-m
C 45	13.4	17.4	17	1	ABT38020	Tumour suppression
C 46	13.4	17.4	17	1	ADC04444	Human Na/H exchang
C 47	13.4	17.4	17	1	ADC04445	Human Na/H exchang
C 48	13.4	17.4	17	1	ADB45419	Tumour suppression
C 49	13.4	17.4	17	1	ADI51144	Human tumour suppr
C 50	13.4	17.4	17	1	ACC53710	Human tumour suppr
C 51	13.4	17.4	17	1	ACN73126	Human GDMPL-1 prob
C 52	13.2	17.1	18	1	AAQ55741	LCR Oligo A. Synt
C 53	13.2	17.1	18	1	AAQ55744	LCR Oligo D. Synt
C 54	13.2	17.1	18	1	AAT14934	Oligo A probe for
C 55	13.2	17.1	18	1	AAT14937	Oligo D probe for
C 56	13.2	17.1	18	1	AAD13161	Human MTSPI protea
C 57	13.2	17.1	18	1	AAD36932	Human MTSPI protea
C 58	13.2	17.1	18	1	ADA25180	Human MTSPI sense
C 59	13.2	17.1	18	1	ADM57469	M. tuberculosis PC
C 60	13	16.9	15	1	ADJ82396	KLMSY-encoding nuc
C 61	13	16.9	17	1	ABN10031	Human GDMPL-1 17-m
C 62	13	16.9	17	1	ACN73121	Human GDMPL-1 prob
C 63	13	16.9	18	1	AAZ35522	PCR primer used to
C 64	12.8	16.6	17	1	ADC04442	Human Na/H exchang
C 65	12.8	16.6	17	1	ADB45336	Tumour suppression
C 66	12.8	16.6	18	1	AAC68677	Chick R35 RNA fing
C 67	12.8	16.6	18	1	ADG14616	Human CTLA-4 exon
C 68	12.8	16.6	18	1	ADL25789	Human cancer suppr
C 69	12.8	16.6	18	1	ADR74794	Allele specific pr
C 70	12.4	16.1	15	1	ADV37028	Human anti-HER2 NC
C 71	12.4	16.1	17	1	ADV64524	Human Her2 class I
C 72	12.4	16.1	17	1	ABN10037	Human GDMPL-1 17-m
C 73	12.4	16.1	17	1	ABZ65329	Human HER2 DNzyme
C 74	12.4	16.1	17	1	ADC04446	Human Na/H exchang
C 75	12.4	16.1	17	1	ADC04441	Human Na/H exchang
C 76	12.4	16.1	17	1	ADC04440	Human Na/H exchang
C 77	12.4	16.1	17	1	ADI47813	Human tumour suppr
C 78	12.4	16.1	17	1	ABE58478	Human VEGF recepto
C 79	12.4	16.1	17	1	ACN73127	Human GDMPL-1 prob
C 80	12.4	16.1	17	1	ADX59138	Human liver cancer
C 81	12.4	16.1	17	1	ADZ34403	Human HER2 substra
C 82	12.2	15.8	17	1	AAA23004	Integrin subunit b
C 83	12.2	15.8	17	1	ADV05926	Human BACE DNzyme
C 84	12.2	15.8	17	1	ADV05924	Human BACE DNzyme
C 85	12.2	15.8	17	1	ADV04194	Human BACE G-cleav
C 86	12.2	15.8	17	1	ADV06876	Human BACE ambery
C 87	12.2	15.8	17	1	ACN05922	WNV Amberzyme subs
C 88	12.2	15.8	17	1	ACN11559	NFKB sub-unit modu
C 89	12.2	15.8	17	1	ACA09006	WNV minus strand I
C 90	12.2	15.8	17	1	ADA99321	Human MD23 scannin
C 91	12.2	15.8	17	1	ACC67819	Murine oligonucleo
C 92	12.2	15.8	17	1	ABE61480	Human VEGF recepto
C 93	12.2	15.8	17	1	ADM84037	DNA detection exte
C 94	12	15.6	12	1	ADM56305	Mouse SLC26A6 anio
C 95	12	15.6	16	1	ADR70044	Human survivin gen
C 96	12	15.6	16	1	ADM10034	Human survivin ant
C 97	12	15.6	16	1	ADM09555	Human survivin ant
C 98	12	15.6	16	1	ADM10035	Human survivin ant
C 99	12	15.6	16	1	ADM10037	Human survivin ant
C 100	12	15.6	16	1	ADM10036	Human survivin ant
C 101	12	15.6	17	1	ABN10030	Human GDMPL-1 17-m
C 102	12	15.6	17	1	ACN73120	Human GDMPL-1 prob
C 103	11.8	15.3	15	1	AAH18889	UCP3 polymorphism
C 104	11.8	15.3	15	1	AAFS2028	IGF-1 oligonucleot
C 105	11.8	15.3	15	1	ABL53810	Equine infectious
C 106	11.8	15.3	15	1	AAS19731	ASO probe #28 to d

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OM nucleic - nucleic search, using sw model

Run on: April 19, 2006, 16:10:20 ; Search time 0.001 Seconds
(without alignments)
225.302 Million cell updates/sec

Title: US-10-643-038-17_994-1070

Perfect score: 77

Sequence: 1 caacaagacggcctggga.....gaagctgatctctgtcaag 77

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 0.5

Searched: 100 seqs, 1463 residues

Total number of hits satisfying chosen parameters: 200

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : issdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	28.2	36.6	33	1	US-08-186-895-4
C 2	21	27.3	21	1	US-07-847-055A-13
C 3	21	27.3	21	1	US-08-403-888A-59
C 4	16	20.8	20	1	PCT-US96-09009-9
C 5	14.8	19.2	21	1	US-09-581-831-3
C 6	14.4	18.7	17	1	US-09-866-108A-10026
C 7	14.4	18.7	17	1	US-09-866-108A-10027
C 8	14.4	18.7	17	1	US-09-205-860-40
C 9	14	18.2	17	1	US-09-866-108A-10024
C 10	14	18.2	17	1	US-09-866-108A-10025
C 11	13.4	17.4	17	1	US-09-866-108A-10028
C 12	13.2	17.1	18	1	US-08-096-947-14
C 13	13.2	17.1	18	1	US-08-096-947-17
C 14	13.2	17.1	18	1	US-07-919-1408-14
C 15	13.2	17.1	18	1	US-07-919-1408-17
C 16	13.2	17.1	18	1	US-08-916-232-14
C 17	13.2	17.1	18	1	US-08-916-232-17
C 18	13.2	17.1	18	1	US-09-657-386B-6
C 19	13.2	17.1	18	1	PCT-US93-06939-14
C 20	13.2	17.1	18	1	PCT-US93-06939-17
C 21	13	16.9	17	1	US-09-866-108A-10023
C 22	12.4	16.1	17	1	US-09-474-432B-817
C 23	12.4	16.1	17	1	US-09-476-387-816
C 24	12.4	16.1	17	1	US-09-866-108A-10029
C 25	12	15.6	17	1	US-09-866-108A-10022
C 26	11.8	15.3	16	1	US-09-371-772B-6986
C 27	11.8	15.3	16	1	5168062-12
C 28	11.8	15.3	16	1	Patent No. 5168062
C 29	11.2	14.8	16	1	US-08-173-489C-4
C 30	11.2	14.5	16	1	US-08-308-892A-12
C 31	11.2	14.5	16	1	US-09-060-299-450
C 32	11.2	14.5	16	1	US-09-402-923A-450
C 33	11.2	14.5	16	1	US-09-798-542-9
C 34	11.2	14.5	16	1	US-09-875-453B-65
C 35	11.1	14.3	15	1	US-08-363-240A-116
C 36	10.8	14.0	15	1	US-08-182-368A-186
C 37	10.8	14.0	15	1	US-08-319-492B-357
C 38	10.8	14.0	15	1	US-08-319-492B-358
C 39	10.8	14.0	15	1	US-08-291-932A-373
C 40	10.8	14.0	15	1	US-08-774-306A-186
C 41	10.8	14.0	15	1	US-09-064-156A-186
C 42	10.4	13.5	13	1	US-08-282-197C-36
C 43	10	13.0	10	1	US-08-171-385-28
C 44	10	13.0	10	1	US-08-351-748-13
C 45	10	13.0	10	1	US-08-430-536A-13
C 46	10	13.0	10	1	US-08-463-660-14
C 47	10	13.0	10	1	US-08-678-280-14
C 48	10	13.0	10	1	US-08-582-261A-4
C 49	10	13.0	10	1	US-08-684-547-13
C 50	10	13.0	10	1	US-08-942-819-3
C 51	10	13.0	10	1	US-08-361-441B-28
C 52	10	13.0	10	1	US-09-016-540-4
C 53	10	13.0	10	1	US-09-308-984-3
C 54	10	13.0	10	1	US-09-313-221A-132
C 55	10	13.0	10	1	US-09-522-955A-3
C 56	10	13.0	10	1	PCT-US93-02246-13
C 57	10	13.0	13	1	US-09-674-913B-14
C 58	10	13.0	14	1	US-08-221-368-2
C 59	10	13.0	14	1	US-08-567-196-2
C 60	10	13.0	14	1	US-08-985-162-1837
C 61	10	13.0	14	1	US-09-401-063-1837
C 62	9.8	12.7	13	1	US-08-615-961-8
C 63	9.8	12.7	13	1	US-08-867-820A-49
C 64	9.8	12.7	13	1	US-08-729-601A-7
C 65	9.8	12.7	13	1	US-08-679-645-1247
C 66	9.8	12.7	14	1	US-08-233-608-26
C 67	9.8	12.7	14	1	US-08-271-880A-49
C 68	9.8	12.7	14	1	US-08-887-480-26
C 69	9.8	12.7	14	1	US-08-485-689-62
C 70	9.8	12.7	14	1	US-08-476-021A-62
C 71	9.8	12.7	14	1	US-08-478-608B-62
C 72	9.8	12.7	14	1	US-08-722-187-26
C 73	9.8	12.7	14	1	US-08-910-408-49
C 74	9.8	12.7	14	1	US-08-985-162-1769
C 75	9.8	12.7	14	1	US-09-249-215-49
C 76	9.8	12.7	14	1	US-08-476-423A-62
C 77	9.8	12.7	14	1	US-09-135-020-99
C 78	9.8	12.7	14	1	US-09-135-010A-99
C 79	9.8	12.7	14	1	US-09-373-845-19
C 80	9.8	12.7	14	1	US-09-444-871-99
C 81	9.8	12.7	14	1	US-09-081-646-24
C 82	9.8	12.7	14	1	US-09-597-735-99
C 83	9.8	12.7	14	1	US-09-444-295-99
C 84	9.8	12.7	14	1	US-09-597-732-99
C 85	9.8	12.7	14	1	US-09-597-731-99
C 86	9.8	12.7	14	1	US-09-401-063-1769
C 87	9.8	12.7	14	1	PCT-US95-04712-26
C 88	9.4	12.2	11	1	US-08-173-489C-331
C 89	9.4	12.2	12	1	US-09-940-244-415
C 90	9.4	12.2	13	1	US-08-738-944-39
C 91	9.4	12.2	13	1	US-08-468-037A-26
C 92	9.4	12.2	13	1	US-08-471-973A-26
C 93	9.4	12.2	13	1	US-09-035-357-26
C 94	9.4	12.2	13	1	US-09-263-352-30
C 95	9.4	12.2	13	1	US-08-936-166-6
C 96	9.4	12.2	13	1	US-09-135-202-26
C 97	9.4	12.2	13	1	US-09-474-432B-141
C 98	9.4	12.2	13	1	US-09-389-283-26
C 99	9.4	12.2	13	1	US-09-476-387-141
C 100	9.4	12.2	13	1	US-10-042-819-8

ALIGNMENTS

RESULT 1

US-08-186-895-4/c

; Sequence 4, Application US/08186895

; Patent No. 553885

; GENERAL INFORMATION:

; APPLICANT: Hollis, Melvyn

; APPLICANT: Needham, Maurice R.C.

; APPLICANT: Gooding, Clare

; APPLICANT: Grosveld, Franklin G.

; TITLE OF INVENTION: Expression Systems

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cushman, Darby & Cushman

; STREET: 1615 L Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/186,895

; FILING DATE: 27-JAN-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/046,383

; FILING DATE: 09-APR-1993

; APPLICATION NUMBER: US/07/810,414

; ATTORNEY/AGENT INFORMATION:

; NAME: Kokulis, Paul N.

; REGISTRATION NUMBER: 16,773

; REFERENCE/DOCKET NUMBER: FWK/3893/93802/MJW

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 33 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-186-895-4

Query Match 36.6%; Score 28.2; DB 1; Length 33;

Best Local Similarity 90.9%; Pred. No. 0.082;

Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GACGGCTGGGATACAACTCTGGAGTCTCTG 40

Db 33 GACGGCTGGGATACAACTCTGGAGTCTCTG 1

RESULT 2

US-07-847-055A-13/c

; Sequence 13, Application US/07847055A

; Patent No. 5530114

; GENERAL INFORMATION:

; APPLICANT: ISIS Pharmaceuticals

; TITLE OF INVENTION: Oligonucleotide Modulation of

; TITLE OF INVENTION: Arachidonic Acid Metabolism

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn

; ADDRESSEE: Kurtz Mackiewicz & No. 5530114ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: WORDPERFECT 5.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/847,055A

; FILING DATE: 19920403

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/516,969

; FILING DATE: April 30, 1990

; ATTORNEY/AGENT INFORMATION:

; NAME: John W. Caldwell

; REGISTRATION NUMBER: 28,937

; REFERENCE/DOCKET NUMBER: ISIS-182

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; ANTI-SENSE: yes

US-07-847-055A-13

Query Match 27.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.94;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATCAACTCTGGAGTCTCTG 40

Db 21 ATCAACTCTGGAGTCTCTG 1

RESULT 3

US-08-403-888A-59/c

; Sequence 59, Application US/08403888A

; Patent No. 5952490

; GENERAL INFORMATION:

; APPLICANT: Hanecek et al.

; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core

; TITLE OF INVENTION: Sequence

; NUMBER OF SEQUENCES: 146

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch disk, 1.44 MB

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 6.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/403,888A

; FILING DATE: 12-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/954,185

; FILING DATE: 29-SEP-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Paul K. Legaard

; REGISTRATION NUMBER: 38,534

; REFERENCE/DOCKET NUMBER: ISIS-1229

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 59:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-403-888A-59
Query Match 27.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATACAACCTCTGGAGTCCTCTG 40
Db 21 ATACAACCTCTGGAGTCCTCTG 1

RESULT 4
PCT-US96-09009-9/c
; Sequence 9, Application PC/TUS9609009
; GENERAL INFORMATION:
; APPLICANT: Buchberg, Arthur M.
; APPLICANT: Siracusa, Linda D.
; APPLICANT: Chepenik, Kenneth P.
; TITLE OF INVENTION: RISK FACTOR FOR COLORECTAL CANCER
; TITLE OF INVENTION: AND
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09009
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,359
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US96-09009-9
Query Match 20.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 CTGATGTCCTGTCAAG 77
Db 20 CTGATGTCCTGTCAAG 5

RESULT 5
US-09-581-831-3
; Sequence 3, Application US/09581831
; Patent No. 6448020
; GENERAL INFORMATION:
; APPLICANT: TOFTGARD, RUNE
; APPLICANT: ZAPHIROPOULOS, PETER G.
; APPLICANT: KOGERMAN, PRIIT
; APPLICANT: GRIMM, THOMAS
; TITLE OF INVENTION: MOLECULES ASSOCIATED WITH THE HUMAN SUPPRESSOR OF FUSED
; TITLE OF INVENTION: GENE
; FILE REFERENCE: 50695-60568
; CURRENT APPLICATION NUMBER: US/09/581,831
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: PCT/SB98/02383
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 9704788-0
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 9802293-2
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-581-831-3
Query Match 19.2%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTGTCA 75
Db 1 GAAGCTGATGTCCTGTCA 18

RESULT 6
US-09-866-108A-10026
; Sequence 10026, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10026
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10026

Query Match      18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42
    |||||
Db 2 TCTGGAGTCTCTGTG 17

RESULT 7
US-09-866-108A-10027
; Sequence 10027, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10027
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10027

Query Match      18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42
    |||||
Db 1 TCTGGAGTCTCTGTG 16

; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10026
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10026

Query Match      18.7%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42
    |||||
Db 1 TCTGGAGTCTCTGTG 16
```

```
RESULT 8
US-09-205-860-40/c
; Sequence 40, Application US/09205860
; Patent No. 5981732
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
; FILE REFERENCE: RTS-0031
; CURRENT APPLICATION NUMBER: US/09/205,860
; CURRENT FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-205-860-40

Query Match      18.7%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 11;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 CCTGGGGATACAACTC 28
    |||||
Db 17 CCTGGGGAGCAACTC 2

RESULT 9
US-09-866-108A-10024
; Sequence 10024, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10024
; LENGTH: 17
; TYPE: DNA
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```

; ORGANISM: Homo sapiens
US-09-866-108A-10024

Query Match      18.2%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCCTCTG 40
Db 4 TCTGGAGTCCTCTG 17

RESULT 10
US-09-866-108A-10025
; Sequence 10025, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: A6MICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: A6MICA Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10025
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10025

Query Match      18.2%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCCTCTG 40
Db 3 TCTGGAGTCCTCTG 16

RESULT 11
US-09-866-108A-10028
; Sequence 10028, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong

```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,947
; FILING DATE: 19930722
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/919,140
; FILING DATE: July 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: STRG 20081 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: 278356
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-08-096-947-14

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACAACCTTGGAGTC 18

RESULT 13
US-08-096-947-17
; Sequence 17, Application US/08096947
; Patent No. 5506137
; GENERAL INFORMATION:
; APPLICANT: Eric J. Mathur
; APPLICANT: Edward J. Marsh
; APPLICANT: Warren E. Schoettlin
; TITLE OF INVENTION: Purified Thermostable
; TITLE OF INVENTION: Pyrococcus Furiosus DNA
; TITLE OF INVENTION: Ligase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,947
; FILING DATE: 19930722
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/919,140
; FILING DATE: July 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: STRG 20081 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,947
; FILING DATE: 19930722
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/919,140
; FILING DATE: July 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: STRG 20081 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: 278356
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-08-096-947-17

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACAACCTTGGAGTC 18

RESULT 14
US-07-919-140B-14/c
; Sequence 14, Application US/07919140B
; Patent No. 5700672
; GENERAL INFORMATION:
; APPLICANT: Eric J. Mathur
; APPLICANT: Edward J. Marsh
; APPLICANT: Warren E. Schoettlin
; TITLE OF INVENTION: Purified Thermostable Pyrococcus
; TITLE OF INVENTION: Furiosus DNA Ligase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/919,140B
; FILING DATE: July 23, 1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; US-07-919-140B-14

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACAACCTTGGAGTC 35
```

Db 18 GGACACAACTTGGAGTC 1

RESULT 15

US-07-919-1408-17
 ; Sequence 17, Application US/079191408
 ; Patent No. 5700872
 ; GENERAL INFORMATION:
 ; APPLICANT: Eric J. Mathur
 ; APPLICANT: Edward J. Marsh
 ; APPLICANT: Warren E. Schoettlin
 ; TITLE OF INVENTION: Purified Thermostable Pyrococcus
 ; TITLE OF INVENTION: Purified Thermostable Pyrococcus
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 2730 Sand Hill Road
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/919.1408
 ; FILING DATE: July 23, 1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Albert P. Halluin
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 8142-013
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-854-3660
 ; TELEFAX: 415-854-3694
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
 ; HYPOTHETICAL: no
 ; ANTI-SENSE: no
 ; US-07-919-1408-17

Query Match 17.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 18;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTTGGAGTC 35
 ||| ||||| |||||
 Db 1 GGACACAACTTGGAGTC 18

RESULT 16

US-08-916-232-14/c
 ; Sequence 14, Application US/08916232
 ; Patent No. 6280998
 ; GENERAL INFORMATION:
 ; APPLICANT: Eric J. Mathur
 ; APPLICANT: Edward J. Marsh
 ; APPLICANT: Warren E. Schoettlin
 ; TITLE OF INVENTION: Purified Thermostable Pyrococcus
 ; TITLE OF INVENTION: Purified Thermostable Pyrococcus
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 2730 Sand Hill Road
 ; CITY: Menlo Park

STATE: California
 COUNTRY: USA
 ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/916,232
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/919,140
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Albert P. Halluin
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 8142-013
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-854-3660
 ; TELEFAX: 415-854-3694
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
 ; HYPOTHETICAL: no
 ; ANTI-SENSE: no
 ; US-08-916-232-14

Query Match 17.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 18;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 18 GGATACAACTTGGAGTC 35
 ||| ||||| |||||
 Db 18 GGACACAACTTGGAGTC 1

RESULT 17

US-08-916-232-17
 ; Sequence 17, Application US/08916232
 ; Patent No. 6280998
 ; GENERAL INFORMATION:
 ; APPLICANT: Eric J. Mathur
 ; APPLICANT: Edward J. Marsh
 ; APPLICANT: Warren E. Schoettlin
 ; TITLE OF INVENTION: Purified Thermostable Pyrococcus
 ; TITLE OF INVENTION: Purified Thermostable Pyrococcus
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 2730 Sand Hill Road
 ; CITY: Menlo Park
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy Disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WordPerfect 5.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/916,232
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/919,140
 ; FILING DATE:

```
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Albert P. Halluin
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: 8142-013
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-854-3660
/ TELEFAX: 415-854-3694
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Chemically Synthesized Oligonucleotide
/ HYPOTHETICAL: no
/ ANTI-SENSE: no
/ US-08-916-232-17

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACAACTTGGAGTC 18

RESULT 18
US-09-657-986B-6/c
/ Sequence 6, Application US/09657986B
/ Patent No. 6797504
/ GENERAL INFORMATION:
/ APPLICANT: Madison, Edwin L.
/ APPLICANT: Semple, Joseph Edward
/ APPLICANT: Coombs, Gary Samuel
/ APPLICANT: Reiner, John Eugene
/ APPLICANT: Ong, Edgar O.
/ APPLICANT: Araldi, Gian Luca
/ TITLE OF INVENTION: Inhibitors of Serine Protease Activity of Matriptase or
/ FILE REFERENCES: Corvas 255/049
/ CURRENT APPLICATION NUMBER: US/09/657,986B
/ CURRENT FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 6
/ LENGTH: 18
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of artificial sequence:
/ US-09-657-986B-6

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 30 GGAGTCCTCTGAGAGTA 47
Db 18 GGAGTCGTAGGAGAGTA 1

RESULT 19
PCT-US93-06939-14/c
/ Sequence 14, Application PC/TUS9306939
/ GENERAL INFORMATION:
/ APPLICANT: Eric J. Mathur
/ APPLICANT: Edward J. Marsh
/ APPLICANT: Warren E. Schoettlin
/ TITLE OF INVENTION: Purified Thermostable
/ TITLE OF INVENTION: Pyrococcus Furiosus DNA
```

```
/ TITLE OF INVENTION: Ligase
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Limbach & Limbach
/ STREET: 2001 Ferry Building
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/06939
/ FILING DATE: 19930722
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/919,140
/ FILING DATE: July 23, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Albert P. Halluin
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: STRG 20081 USA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 433-4150
/ TELEFAX: (415) 433-8716
/ TELEX: 278356
/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Chemically Synthesized Oligonucleotide
/ HYPOTHETICAL: no
/ ANTI-SENSE: no
/ PCT-US93-06939-14

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACAACTTGGAGTC 1

RESULT 20
PCT-US93-06939-17
/ Sequence 17, Application PC/TUS9306939
/ GENERAL INFORMATION:
/ APPLICANT: Eric J. Mathur
/ APPLICANT: Edward J. Marsh
/ APPLICANT: Warren E. Schoettlin
/ TITLE OF INVENTION: Purified Thermostable
/ TITLE OF INVENTION: Pyrococcus Furiosus DNA
/ TITLE OF INVENTION: Ligase
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Limbach & Limbach
/ STREET: 2001 Ferry Building
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.0
/ CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: PCT/US93/06939
; FILING DATE: 19930722
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/919,140
; FILING DATE: July 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: STRG 20081 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: 278356
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Chemically Synthesized Oligonucleotide
; HYPOTHETICAL: no
; ANTI-SENSE: no
; PCT-US93-06939-17

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
DB 1 GGACACAACTTGGAGTC 18

RESULT 21
US-09-866-108A-10023
; Sequence 10023, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15/55
; SOFTWARE: Acomica Sequence Listing Engine
```

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; Patent No. 6686188
; SEQ ID NO 10023
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-10023

Query Match 16.9%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCT 39
DB 5 TCTGGAGTCTCTCT 17

RESULT 22
US-09-474-432B-817
; Sequence 817, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 817
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-817

Query Match 16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGGAGTCTCTCTCA 41
DB 4 CUGGAGCCCUUGA 17

RESULT 23
US-09-476-387-816
; Sequence 816, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their incorporation into Oligonucleot
; FILE REFERENCE: MEHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
```

```
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 816
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-476-387-816

Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      28 CTGGAGTCTCTGAG 41
Db      4 CUGGAGCCUCUGA 17
      |:||||| |:|:|

RESULT 24
US-09-866-108A-10029
; Sequence 10029, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10022
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-10022

Query Match      15.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 TCTGGAGTCTCTC 38
Db      6 TCTGGAGTCTCTC 17
      ||||| |||||

RESULT 26
US-09-371-772B-6986/c
; Sequence 6986, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
```

```
Query Match      16.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 23;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      29 TGGAGTCTCTGAG 42
Db      1 TGGAGTCTCTGTG 14
      ||||| |||||

RESULT 25
US-09-866-108A-10022
; Sequence 10022, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 10022
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-10022

Query Match      15.6%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 TCTGGAGTCTCTC 38
Db      6 TCTGGAGTCTCTC 17
      ||||| |||||
```

```
RESULT 26
US-09-371-772B-6986/c
; Sequence 6986, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
```



```
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6986
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-371-772B-6986

Query Match      15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      52 GCCAGCGAGCTGAT 66
Db      16 GCCAGCATAGCTGAT 2

RESULT 27
5168062-12/c
; Patent No. 5168062
; APPLICANT: STINSKI, MARK F.
; TITLE OF INVENTION: TRANSFER VECTORS AND MICROORGANISMS
; CONTAINING HUMAN CYTOMEGALOVIRUS IMMEDIATE-EARLY
; PROMOTER-REGULATORY DNA SEQUENCE
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/582,130
; FILING DATE: 10-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 256,134
; FILING DATE: 5-OCT-1988
; APPLICATION NUMBER: 58,662
; FILING DATE: 22-MAY-1987
; APPLICATION NUMBER: 696,617
; FILING DATE: 30-JAN-1985
; SEQ ID NO:12:
; LENGTH: 16
5168062-12

Query Match      15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      63 TGATGTCCTGTCAG 77
Db      15 TGATGTAAGTCCCAAG 1

RESULT 28
5168062-13/c
; Patent No. 5168062
; APPLICANT: STINSKI, MARK F.
; TITLE OF INVENTION: TRANSFER VECTORS AND MICROORGANISMS
; CONTAINING HUMAN CYTOMEGALOVIRUS IMMEDIATE-EARLY
; PROMOTER-REGULATORY DNA SEQUENCE
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/582,130
; FILING DATE: 10-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 256,134
; FILING DATE: 5-OCT-1988
```

```
; APPLICATION NUMBER: 58,662
; FILING DATE: 22-MAY-1987
; APPLICATION NUMBER: 696,617
; FILING DATE: 30-JAN-1985
; SEQ ID NO:13:
; LENGTH: 16
5168062-13

Query Match      15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      63 TGATGTCCTGTCAG 77
Db      15 TGATGTAAGTCCCAAG 1

RESULT 29
US-08-173-489C-4/c
; Sequence 4, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from c-myc
; DESCRIPTION: sequence region in Seq ID No. 58612443
; HYPOTHETICAL: Yes
; ANTI-SENSE: No
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 4 :FROM 1 TO 16
US-08-173-489C-4

Query Match      14.8%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 32;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      40 GAGAGGTAAAGAG 52
```

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Db      14 GACAGGGAAGAG 2
||||| |||||
STATE: Virginia
COUNTRY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,299
FILING DATE: 15-APR-1998
CLASSIFICATION: 435
TITLE OF INVENTION: SPECIES-SPECIFIC DETECTION OF MYCOBACTERIUM KANSASII
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/308,892A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3128
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-308-892A-12

Query Match      14.5%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 AACAAAGACGGCCTGGG 18
||||| ||||| ||
Db      1 AACTCGAGCGGCTCGG 16

RESULT 31
US-09-060-299-450
; Sequence 450, Application US/09060299
; Patent No. 6545137
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; Hesse, John W
; Caskey, Charles T
; Cox, Roger D
; Gerhold, David
; Hammond, Holly
; Hey, Patricia
; Kawaguchi, Yoshihiko
; Merriman, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. 6545137el Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6545137th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/09/402,923A
; FILING DATE: 14-Feb-2001

Db      1 TCACAGGTAAGGAGCC 16
||||| ||||| |||||
QY      39 TCACAGGTAAGGAGCC 54
||||| ||||| |||||
Db      1 TCACAGGTAAGGAGCC 16

RESULT 32
US-09-402-923A-450
; Sequence 450, Application US/09402923A
; Patent No. 6555654
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; Hesse, John W
; Caskey, Charles T
; Cox, Roger D
; Gerhold, David
; Hammond, Holly
; Hey, Patricia
; Kawaguchi, Yoshihiko
; Merriman, Tony R
; Metzker, Michael L
; TITLE OF INVENTION: No. 6555654el LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. 6555654th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA: US/09/402,923A
; FILING DATE: 14-Feb-2001
```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 450:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 450:
US-09-402-923A-450

Query Match 14.5% Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAGAGCC 54
Db 1 TCACAGGTAAGAGCC 16

RESULT 33
US-09-798-542-g/c
; Sequence 9, Application US/09798542
; Patent No. 6685948
; GENERAL INFORMATION:
; APPLICANT: Zeng, Lingling
; TITLE OF INVENTION: REPLICATION-DEFECTIVE DENGUE VIRUSES
; TITLE OF INVENTION: THAT ARE REPLICATION-DEFECTIVE IN MOSQUITOES FOR USE AS
; TITLE OF INVENTION: VACCINES
; FILE REFERENCE: NIH145.001C1
; CURRENT APPLICATION NUMBER: US/09/798,542
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: PCT/US 99/02598
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: US 60/098,981
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Flavivirus, West Nile
US-09-798-542-9

Query Match 14.5% Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 26 CTCGGAGTCTCTGA 41
Db 16 CTCGTGTCTCTATGA 1

RESULT 34
US-09-875-453B-65/c
; Sequence 65, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungshuh P.
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELEPHONE: (213) 489-1600

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; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.
; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongsachith, Ana T.
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135 US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-875-453B-65

Query Match 14.5% Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 35;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 38 CTGAGAGGTAAGAGC 53
Db 16 CTGGAGGTGGAGGC 1

RESULT 35
US-08-363-240A-116/c
; Sequence 116, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwigen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELEPHONE: (213) 489-1600

```

TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 116:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-363-240A-116

Query Match 14.3%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 GTCCTCTGAGA 43
 Db 15 GTCCTCTGAGA 5

RESULT 36

US-08-182-968A-186/c
 Sequence 186, Application US/08182968A
 Patent No. 5610054
 GENERAL INFORMATION:
 APPLICANT: Draper, Kenneth G.
 TITLE OF INVENTION: METHOD AND REAGENT FOR
 TITLE OF INVENTION: INHIBITING HEPATITIS C
 TITLE OF INVENTION: VIRUS REPLICATION
 NUMBER OF SEQUENCES: 497
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 SUITE: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/182,968A
 FILING DATE: 13-JANUARY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/882,888
 FILING DATE: 14-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 205/277
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 955-0440
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 186:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-182-968A-186

Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 38;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 57 CGAAGCTGATGTC 70
 Db 15 CCAAGATGATGTC 2

RESULT 37

US-08-319-492B-357/c
 Sequence 357, Application US/08319492B
 Patent No. 5616488
 GENERAL INFORMATION:
 APPLICANT: Sullivan, Sean M.
 APPLICANT: Draper, Kenneth G.
 APPLICANT: McSwiggen, James
 APPLICANT: Stinchcomb, Dan T.
 TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
 TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS
 TITLE OF INVENTION: OF IL-5
 NUMBER OF SEQUENCES: 751
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 SUITE: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/319,492B
 FILING DATE: October 7, 1994
 PRIOR APPLICATION DATA:
 APPLICATION DATA: including application
 PRIOR APPLICATION DATA: described below:
 APPLICATION NUMBER: 08/008,895
 FILING DATE: January 19, 1993
 APPLICATION NUMBER: 07/989,849
 FILING DATE: December 7, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 209/276
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 357:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-319-492B-357

Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 38;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 25 ACTCTGAGTCCTC 38
 Db 14 ACTCTGAAGTCCTC 1

RESULT 38

US-08-319-492B-358/c
 Sequence 358, Application US/08319492B
 Patent No. 5616488
 GENERAL INFORMATION:
 APPLICANT: Sullivan, Sean M.
 APPLICANT: Draper, Kenneth G.
 APPLICANT: McSwiggen, James
 APPLICANT: Stinchcomb, Dan T.
 TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES

;; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS

;; TITLE OF INVENTION: OF IL-5

;; NUMBER OF SEQUENCES: 751

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Lyon & Lyon

;; STREET: 633 West Fifth Street

;; CITY: Suite 4700

;; STATE: Los Angeles

;; COUNTRY: California

;; ZIP: U.S.A.

;; ZIP: 90071

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

;; MEDIUM TYPE: storage

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: IBM P.C. DOS 5.0

;; SOFTWARE: Word Perfect 5.1

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/319,492B

;; FILING DATE: October 7, 1994

;; PRIOR APPLICATION DATA:

;; PRIOR APPLICATION DATA: including application

;; PRIOR APPLICATION DATA: described below:

;; APPLICATION NUMBER: 08/008,895

;; FILING DATE: January 19, 1993

;; APPLICATION NUMBER: 07/989,849

;; FILING DATE: December 7, 1992

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Warburg, Richard

;; REGISTRATION NUMBER: 32,327

;; REFERENCE/DOCKET NUMBER: 209/276

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (213) 489-1600

;; TELEFAX: (213) 955-0440

;; TELEX: 67-3510

;; INFORMATION FOR SEQ ID NO: 358:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 15 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; US-08-319-492B-358

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/ FILING DATE: May 14, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 223/227
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 186:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-774-306A-186

Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGTC 70
Db 15 CCAAGATGATGTC 2

RESULT 41
US-09-064-156A-186/c
; Sequence 186, Application US/09064156A
; Patent No. 6132966
; GENERAL INFORMATION:
; APPLICANT: Draper, Kenneth G.
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HEPATITIS C
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 498
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,156A
; FILING DATE: April 21, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/774,306
; FILING DATE: December 26, 1996
; APPLICATION NUMBER: 08/182,968
; FILING DATE: January 13, 1994
; APPLICATION NUMBER: 07/882,888
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
/ TOPOLOGY: linear
/ US-09-064-156A-186

Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 38;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGTC 70
Db 15 CCAAGATGATGTC 2

RESULT 42
US-08-282-197C-36
; Sequence 36, Application US/08282197C
; Patent No. 5871730
; GENERAL INFORMATION:
; APPLICANT: Brzezinski, Ryszard
; APPLICANT: Dery, Claude V
; APPLICANT: Beaulieu, Carole
; TITLE OF INVENTION: Thermostable Xylanase DNA, Protein and
; TITLE OF INVENTION: Methods of Use
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,197C
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cimbala, Michele A
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0410000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-282-197C-36

Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 56 GCGAAGCTGATG 67
Db 2 GCGAGCGUGAUG 13

RESULT 43
US-08-171-385-28
; Sequence 28, Application US/08171385
; Patent No. 5527884
; GENERAL INFORMATION:
; APPLICANT: Mary E. Russell
; APPLICANT: Ulrike Utans
; TITLE OF INVENTION: Mediators of Chronic Allograft
; TITLE OF INVENTION: Rejection
; NUMBER OF SEQUENCES: 32
```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: US/08/171.385
APPLICATION NUMBER: US/08/171.385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-171-385-28

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 44
US-08-351-748-13
Sequence 13 Application US/08351748
Patent No. 5599672
GENERAL INFORMATION:
APPLICANT: Liang, Peng
APPLICANT: Bianchi, Cesario P.
TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
TITLE OF INVENTION: MESSENGER RNAS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL & STEWART
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/351.748
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/033.084

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: US/08/171.385
APPLICATION NUMBER: US/08/171.385
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/006001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-171-385-28

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 45
US-08-430-536A-13
Sequence 13 Application US/08430536A
Patent No. 566547
GENERAL INFORMATION:
APPLICANT: Liang, Peng
APPLICANT: Pardee, Arthur B.
TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
TITLE OF INVENTION: MESSENGER RNAS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL & STEWART
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430.536A
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Herschbach Ph.D., Brenda M.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 181411-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-430-536A-13

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 45
US-08-430-536A-13
Sequence 13 Application US/08430536A
Patent No. 566547
GENERAL INFORMATION:
APPLICANT: Liang, Peng
APPLICANT: Pardee, Arthur B.
TITLE OF INVENTION: IDENTIFYING, ISOLATING, AND CLONING
TITLE OF INVENTION: MESSENGER RNAS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHOATE, HALL & STEWART
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430.536A
FILING DATE: 25-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Herschbach Ph.D., Brenda M.
REGISTRATION NUMBER: 39,223
REFERENCE/DOCKET NUMBER: 181411-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-430-536A-13

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 46
US-08-463-660-14
; Sequence 14, Application US/08463660
; Patent No. 5759776
; GENERAL INFORMATION:
; APPLICANT: SMITH, HELENE S.
; APPLICANT: CHEN, LING-CHUN
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,660
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 28888-20001.00
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-463-660-14

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 47
US-08-678-280-14
; Sequence 14, Application US/08678280
; Patent No. 5776683
; GENERAL INFORMATION:
; APPLICANT: SMITH, HELENE S.
; APPLICANT: CHUN, LING-CHEN
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND
; TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/678,280
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 28888-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-678-280-14

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 48
US-08-582-261A-4
; Sequence 4, Application US/08582261A
; Patent No. 5817461
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard C.
; APPLICANT: Hirsh, Jack
; APPLICANT: Weitz, Jeff
; TITLE OF INVENTION: Methods and Compositions for Diagnosis
; TITLE OF INVENTION: of Hyperhomocysteinemia
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/582,261A
; FILING DATE: 03-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 016558-001200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
US-08-562-261A-4

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
DB 1 AGCCAGCGAA 10
|||||

RESULT 49
US-08-684-547-13
; Sequence 13, Application US/08684547
; Patent No. 5965409
; GENERAL INFORMATION:
; APPLICANT: Pardee Ph.D., Arthur B.
; APPLICANT: Liang Ph.D., Peng
; TITLE OF INVENTION: SYSTEM FOR COMPARING LEVELS OR AMOUNTS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,547
; FILING DATE: 19-JUL-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0181411-0013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248-4000
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-684-547-13

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
DB 1 AGCCAGCGAA 10
|||||

RESULT 50
US-08-942-819-3
; Sequence 3, Application US/08942819
; Patent No. 5965707
; GENERAL INFORMATION:
; APPLICANT: Tam, See-ying
; APPLICANT: Tsai, Mindy
; APPLICANT: Galli, Stephen J.
; TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF

```

```
/ FILING DATE: 21-DEC-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fraser, Janis K.
/ REGISTRATION NUMBER: 34,819
/ REFERENCE/DOCKET NUMBER: 05433/014001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/542-5070
/ TELEFAX: 617/542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 28:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-361-441B-28

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 52
US-09-016-540-4
/ Sequence 4, Application US/09016540
/ Patent No. 6132965
/ GENERAL INFORMATION:
/ APPLICANT: Austin, Richard C.
/ APPLICANT: Hirsh, Jack
/ APPLICANT: Weitz, Jeff
/ TITLE OF INVENTION: Methods and Compositions for Diagnosis
/ TITLE OF INVENTION: of Hyperhomocysteinemia
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, 8th Floor
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/016,540
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/582,261
/ FILING DATE: 03-JAN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Heslin, James M.
/ REGISTRATION NUMBER: 29,541
/ REFERENCE/DOCKET NUMBER: 016558-001200US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-576-0200
/ TELEFAX: 415-576-0300
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-016-540-4

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
```

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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 53
US-09-308-984-3
/ Sequence 3, Application US/09308984
/ Patent No. 6388065
/ GENERAL INFORMATION:
/ APPLICANT: Durst, Matthias
/ APPLICANT: Nees, Matthias
/ TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
/ FILE REFERENCE: SCHU 204 (09902857)
/ CURRENT APPLICATION NUMBER: US/09/308,984
/ CURRENT FILING DATE: 1999-09-03
/ PRIOR APPLICATION NUMBER: PCT/DE97/02660
/ PRIOR FILING DATE: 1996-11-12
/ PRIOR APPLICATION NUMBER: DE 196 49207
/ PRIOR FILING DATE: 1997-11-27
/ NUMBER OF SEQ ID NOS: 4
/ SEQ ID NO 3
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/
US-09-308-984-3

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 54
US-09-313-221A-132
/ Sequence 132, Application US/09313221A
/ Patent No. 6468743
/ GENERAL INFORMATION:
/ APPLICANT: Thomas L. Romick (Inventor)
/ APPLICANT: Mark S. Fraser (Inventor)
/ TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL
/ TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS
/ FILE REFERENCE: HUNT-042784
/ CURRENT APPLICATION NUMBER: US/09/313,221A
/ CURRENT FILING DATE: 1999-05-17
/ PRIOR APPLICATION NUMBER: US 60/086,025
/ PRIOR FILING DATE: 1998-05-18
/ NUMBER OF SEQ ID NOS: 145
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 132
/ LENGTH: 10
/ TYPE: DNA
/ ORGANISM: Compylobacter jejuni
/
US-09-313-221A-132

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10

RESULT 55
US-09-522-955A-3
/ Sequence 3, Application US/09522955A
/ Patent No. 6500942
```

GENERAL INFORMATION:
; APPLICANT: Tam, See-Ying
; APPLICANT: Tsai, Mindy
; APPLICANT: Galli, Stephen J.
; TITLE OF INVENTION: RIN2, A NOVEL INHIBITOR OF RAS-MEDICATED
; TITLE OF INVENTION: SIGNALING
; FILE REFERENCE: 1440.1089-004
; CURRENT APPLICATION NUMBER: US/09/522,955A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: PCT/US98/19056
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: US 08/942,819
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: US 60/058,520
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-522-955A-3

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
|||||
Db 1 AGCCAGCGAA 10

RESULT 56
PCT-US93-02246-13
; Sequence 13, Application PC/TUS9302246
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; APPLICANT: Pardee, Arthur B.
; TITLE OF INVENTION: Identifying, Isolating and Cloning
; TITLE OF INVENTION: Messenger RNAs
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Choate, Hall & Stewart
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02190
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02246
; FILING DATE: 19930311
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/850,343
; FILING DATE: 11-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasternack, Sam
; REGISTRATION NUMBER: 29,576
; REFERENCE/DOCKET NUMBER: DFC1234CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 227-5020
; TELEFAX: 617 227-7566
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: NUCLEIC ACID

STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US93-02246-13

Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
|||||
Db 1 AGCCAGCGAA 10

RESULT 57
US-09-674-913B-14
; Sequence 14, Application US/09674913B
; Patent No. 6861057
; GENERAL INFORMATION:
; APPLICANT: Gaudernack, Gustav
; APPLICANT: Eriksen, Jon Amund
; APPLICANT: Moller, Mona
; TITLE OF INVENTION: Frameshift Mutants of Beta-Amyloid Precursor Protein and Ubiquitin
; TITLE OF INVENTION: Their Use
; FILE REFERENCE: 001702.401600
; CURRENT APPLICATION NUMBER: US/09/674,913B
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/NO99/00141
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: NO 19982098
; PRIOR FILING DATE: 1998-05-08
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-674-913B-14

Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TCTGAGAGGT 46
|||||
Db 1 TCTGAGAGGT 10

RESULT 58
US-08-221-968-2/c
; Sequence 2, Application US/08221968
; Patent No. 5472843
; GENERAL INFORMATION:
; APPLICANT: Millman, Curt L.
; TITLE OF INVENTION: NUCLEIC ACID PROBES TO HAEMOPHILUS INFLUENZAE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,968
; FILING DATE:

```
/ CLASSIFICATION: 435
/ PRIOR APPLICATION NUMBER: US 07/690,788
/ FILING DATE: 25-APR-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 193/119
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 213-489-1600
/ TELEFAX: 213-955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 bases
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-221-968-2

Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AGCGAAGCTG 64
Db 12 AGCGAAGCTG 3

RESULT 59
US-08-567-196-2/c
; Sequence 2, Application US/08567196
; Patent No. 5830654
; GENERAL INFORMATION:
; APPLICANT: Milliman, Curt L.
; TITLE OF INVENTION: NUCLEIC ACID PROBES TO HAEMOPHILUS
; TITLE OF INVENTION: INFLUENZA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,196
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/690,788
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/119
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 213-489-1600
; TELEFAX: 213-955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
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US-08-567-196-2

Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AGCGAAGCTG 64
Db 12 AGCGAAGCTG 3

RESULT 60
US-08-985-162-1837/c
; Sequence 1837, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1837:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-985-162-1837

Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGAGCCAGCG 58
Db 14 AGAGCCAGCG 5

RESULT 61
US-09-401-063-1837/c
; Sequence 1837, Application US/09401063
```

; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Seghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggan, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/401,063
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/985,162
; FILING DATE: 04 December 1997
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1837:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-401-063-1837

Query Match 13.0%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 AGAGCCGCG 58
Db 14 AGAGCCGCG 5

RESULT 62
US-08-615-961-8
; Sequence 8, Application US/08615961
; Patent No. 5877162
; GENERAL INFORMATION:
; APPLICANT: Martina Werner and Shaji T. George
; TITLE OF INVENTION: Short External Guide Sequences
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA

; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,961
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: IL1115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-615-961-8

Query Match 12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 69.2%; Pred. No. 48;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 GGCCTGGGGATAC 23
Db 1 GGUUGGGGAUAC 13

RESULT 63
US-08-867-820A-49/c
; Sequence 49, Application US/08867820A
; Patent No. 5891685
; GENERAL INFORMATION:
; APPLICANT: YAMAGISHI Masahiro
; APPLICANT: TAKAI Yukie
; APPLICANT: MIKAWA Takashi
; APPLICANT: HARA Mari
; APPLICANT: UEDA Makoto
; APPLICANT: OHARA Akiko
; TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S) - -HALOGENATED- -HYDROXYBUTY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,820A
; FILING DATE: June 3, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 1416/OP574US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; INFORMATION FOR SEQ ID NO: 49:

```
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ ORIGINAL SOURCE:
/ ORGANISM: Selenophoma donacis
/ STRAIN: CBS417.51
US-08-867-820A-49

Query Match 12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 60 AGCTGAGTCTCG 72
Db 13 AGCTGAGTCTG 1

RESULT 64
US-08-729-601A-7/c
/ Sequence 7, Application US/08729601A
/ Patent No. 6166302
/ GENERAL INFORMATION:
/ APPLICANT: Merlo, Donald J.
/ TITLE OF INVENTION: Modified Bacillus Thuringiensis Gene for
/ TITLE OF INVENTION: Lepidopteran Control in Plants
/ NUMBER OF SEQUENCES: 84
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fitch, Even, Tabin & Flannery
/ STREET: 135 S. LaSalle St.
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60603
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/729,601A
/ FILING DATE:
/ CLASSIFICATION: 80
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Krueger, James P.
/ REGISTRATION NUMBER: 35,234
/ REFERENCE/DOCKET NUMBER: 60089
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-372-7842
/ TELEFAX: 312-372-7848
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
US-08-729-601A-7

Query Match 12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 CTCTGAGTCTCTC 38
Db 13 CTCTAGAGTCCCC 1

RESULT 65
US-08-679-645-1247/c
/ Sequence 1247, Application US/08679645
/ Patent No. 6350934
/ GENERAL INFORMATION:
/ APPLICANT: Zwick, Michael G.
/ APPLICANT: Edington, Brent E.
/ APPLICANT: McSwiggen, James A.
/ APPLICANT: Merlo, Patricia Ann Owens
/ APPLICANT: Guo, Lining
/ APPLICANT: Skokut, Thomas A.
/ APPLICANT: Young, Scott A.
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Merlo, Donald J.
/ TITLE OF INVENTION: COMPOSITION AND METHODS FOR
/ TITLE OF INVENTION: MODULATION OF GENE EXPRESSION
/ TITLE OF INVENTION: IN PLANTS
/ NUMBER OF SEQUENCES: 1263
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/679,645
/ FILING DATE: July 12, 1996
/ CLASSIFICATION: 80
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/001,135
/ FILING DATE: July 13, 1995
/ APPLICATION NUMBER: 08/300,726
/ FILING DATE: September 2, 1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 219/247
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 1247:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-679-645-1247

Query Match 12.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 48;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 26 CTCTGAGTCTCTC 38
Db 13 CTCTAGAGTCCCC 1

RESULT 66
US-08-233-608-26/c
/ Sequence 26, Application US/08233608
/ Patent No. 5585238
/ GENERAL INFORMATION:
/ APPLICANT: Ligon, James M
/ APPLICANT: Beck, James J
/ TITLE OF INVENTION: Detection of Fungal Pathogens Using the
/ TITLE OF INVENTION: Polymerase Chain Reaction
```

```
;
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/233,608
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spullin, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer JB443
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-233-608-26

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AGACGGCCTCGG 19
Db 13 AGACGGCCTCGG 1

RESULT 67
US-08-271-880A-49/c
; Sequence 49, Application US/08271880A
; Patent No. 5693535
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; APPLICANT: Bharat Chowhiza
; APPLICANT: James McSwiggen
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James D. Thompson
; TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
; TITLE OF INVENTION: REPLICATION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ Version 1.5
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,880A
; FILING DATE: July 7, 1994
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: two
; APPLICATION NUMBER: 08/103,243
; FILING DATE: August 6, 1993
; APPLICATION NUMBER: 07/882,886
; FILING DATE: May 14, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 206/116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-271-880A-49

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCT 71
Db 14 AAGCTGATGTCCT 2

RESULT 68
US-08-887-480-26/c
; Sequence 26, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSES: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer JB443
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-887-480-26

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGG 19
Db 13 AGACGGCTCCG 1

RESULT 69
US-08-485-689-62/c
; Sequence 62, Application US/08485689
; Patent No. 5856188
; GENERAL INFORMATION:
; APPLICANT: Hampel, Arnold E.
; APPLICANT: Tritz, Richard H.
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States Of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,689
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43863-CLX/JPW/KJP
; TELEPHONE: 212-278-0400
; TELEFAX: 212-278-0526
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-485-689-62

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACAAGACGGCC 14
Db 14 AAACAGGACGGTC 2

RESULT 70
US-08-476-021A-62/c
; Sequence 62, Application US/08476021A
; Patent No. 5858785
; GENERAL INFORMATION:
; APPLICANT: Hampel, Arnold E.
; APPLICANT: Tritz, Richard H.
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States Of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,608B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678

; APPLICANT: Hampel, Arnold E.
; APPLICANT: Tritz, Richard H.
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States Of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,021A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43863-DZ/JPW/KJP
; TELEPHONE: 212-278-0400
; TELEFAX: 212-278-0526
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-476-021A-62

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAACAAGACGGCC 14
Db 14 AAACAGGACGGTC 2

RESULT 71
US-08-478-608B-62/c
; Sequence 62, Application US/08478608B
; Patent No. 5869339
; GENERAL INFORMATION:
; APPLICANT: Hampel, Arnold E.
; APPLICANT: Tritz, Richard H.
; TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States Of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,608B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 43863-C1Z/JPW/KJP
 TELEPHONE: 212-278-0400
 TELEFAX: 212-278-0526
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA (genomic)
 US-08-478-608B-62

Query Match 12.7%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 51;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAACAGACGGCC 14
 Db 14 AAACAGACGGTC 2

RESULT 72
 US-08-722-187-26/c

Sequence 26, Application US/08722187
 Patent No. 5955274
 GENERAL INFORMATION:
 APPLICANT: Ligon, James M
 APPLICANT: Beck, James J
 TITLE OF INVENTION: Detection of Fungal Pathogens Using the
 TITLE OF INVENTION: Polymerase Chain Reaction
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ciba-Geigy Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: NY
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/722,187
 FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/233,608
 FILING DATE: 04-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Waleh, Andrea C.
 REGISTRATION NUMBER: 34,988
 REFERENCE/DOCKET NUMBER: CGC 1739
 TELEPHONE: 919-541-8666
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: Oligonucleotide primer JB443
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-722-187-26

Query Match 12.7%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 51;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGGGG 19
 Db 13 AGACGGCCTCGG 1

RESULT 73

US-08-910-408-49/c
 Sequence 49, Application US/08910408
 Patent No. 5972704

GENERAL INFORMATION:
 APPLICANT: Kenneth G. Draper
 APPLICANT: Bharat Chowrira
 APPLICANT: James McSwiggen
 APPLICANT: Dan T. Stinchcomb
 APPLICANT: James D. Thompson
 TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
 TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS
 TITLE OF INVENTION: REPLICATION
 NUMBER OF SEQUENCES: 232
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: Storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/910,408
 FILING DATE:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/271,880
 FILING DATE: July 7, 1994
 APPLICATION NUMBER: 08/103,243
 FILING DATE: August 6, 1993
 APPLICATION NUMBER: 07/882,886
 FILING DATE: May 14, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 206/116
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-910-408-49

Query Match 12.7%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 51;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCT 71
 Db 14 AAGCTGATGTCCT 2

RESULT 74

US-08-985-162-1769
 Sequence 1769, Application US/08985162
 Patent No. 6057156

GENERAL INFORMATION:
APPLICANT: Akhtar, Saghir
APPLICANT: Fell, Patricia
APPLICANT: McSwiggen, James
TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT
TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
TITLE OF INVENTION: FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1877
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,162
FILING DATE: 04 December 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/036,476
FILING DATE: 31 January 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/107
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1769:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-985-162-1769

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GACGGCCTGGGA 20
Db 2 GACGGCGGGGCA 14

RESULT 75
US-09-249-215-49/c
Sequence 49, Application US/09249215
Patent No. 6159692
GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
Bharat Chowrira
James McSwiggen
Dan T. Stinchcomb
James D. Thompson
TITLE OF INVENTION: METHOD AND REAGENT FOR INHIBITING
HUMAN IMMUNODEFICIENCY VIRUS
REPLICATION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,215
FILING DATE: 12-Feb-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,408
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/103,243
FILING DATE: August 6, 1993
APPLICATION NUMBER: 07/882,886
FILING DATE: May 14, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 206/116
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-249-215-49

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCT 71
Db 14 AAGCTGGTGTCT 2

RESULT 76
US-08-476-423A-62/c
Sequence 62, Application US/08476423A
Patent No. 6221661
GENERAL INFORMATION:
APPLICANT: Hampel, Arnold E.
APPLICANT: Tritz, Richard H.
TITLE OF INVENTION: RNA CATALYST FOR CLEAVING SPECIFIC RNA SEQUENCES
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,423A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.

```

; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 43863-C2/JPW/KJP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-278-0526
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-476-423A-62

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 AAACAAGCGCC 14
Db  14 AAACAGGCGTC 2

RESULT 77
US-09-135-020-99
; Sequence 99, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/135,020
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-020-99

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 AAACAAGCGCC 14
Db  14 AAACAGGCGTC 2

RESULT 77
US-09-135-020-99
; Sequence 99, Application US/09135020
; Patent No. 6274332
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/135,020
; CURRENT FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-135-020-99

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  34 TCCTCTGAGAGGT 46
Db  2 TCCTTTAAGAGGT 14

RESULT 79
US-09-373-845-19
; Sequence 19, Application US/09373845
; Patent No. 6316230
; GENERAL INFORMATION:
; APPLICANT: The Perkin-Elmer Corporation
; TITLE OF INVENTION: POLYMERASE EXTENSION AT 3' TERMINUS OF PNA-DNA CHIMERA
; FILE REFERENCE: 4468 US
; CURRENT APPLICATION NUMBER: US/09/373,845
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Bacterial
US-09-373-845-19

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  4 ACAAGACGGCTG 16
Db  1 ACACGACGGCCAG 13

RESULT 80
US-09-444-871-99
; Sequence 99, Application US/09444871
; Patent No. 6323026
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN minK WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,871
; CURRENT FILING DATE: 1999-11-22

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; EARLIER APPLICATION NUMBER: US 09/135,020
; EARLIER FILING DATE: 1998-08-17
; CURRENT FILING DATE: 2000-06-19
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-871-99

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 81
US-09-081-646-24
; Sequence 24, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Zhang, Lin
; APPLICANT: Zhou, Wei
; TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
; FILE REFERENCE: 01107, 74664
; CURRENT APPLICATION NUMBER: US/09/081,646
; CURRENT FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: 60/047,352
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 871
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-081-646-24

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 65 ATGTCCTGTCAAG 77
Db 2 ATGTCCTATTAAAG 14

RESULT 82
US-09-597-735-99
; Sequence 99, Application US/09597735
; Patent No. 6420124
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Curran, Mark E.
; APPLICANT: Landes, Gregory M.
; APPLICANT: Comore, Timothy D.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE

; FILE REFERENCE: 2323-133
; CURRENT APPLICATION NUMBER: US/09/597,735
; CURRENT FILING DATE: 2000-06-19
; EARLIER APPLICATION NUMBER: 09/135,010
; EARLIER FILING DATE: 1998-08-17
; EARLIER APPLICATION NUMBER: 60/094,477
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: 08/921,068
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 08/739,383
; EARLIER FILING DATE: 1996-10-29
; EARLIER APPLICATION NUMBER: 60/019,014
; EARLIER FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-597-735-99

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 83
US-09-444-295-99
; Sequence 99, Application US/09444295
; Patent No. 6432644
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Sanguinetti, Michael C.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN THE KCNE1 GENE ENCODING HUMAN mink WHICH
; TITLE OF INVENTION: CAUSE ARRHYTHMIA SUSCEPTIBILITY THEREBY ESTABLISHING
; TITLE OF INVENTION: KCNE1 AS AN LQT GENE
; FILE REFERENCE: 2323-131
; CURRENT APPLICATION NUMBER: US/09/444,295
; CURRENT FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/135,020
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 08/921,068
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 08/739,383
; PRIOR FILING DATE: 1996-10-29
; PRIOR APPLICATION NUMBER: 60/019,014
; PRIOR FILING DATE: 1995-12-22
; PRIOR APPLICATION NUMBER: 60/094,477
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-444-295-99

Query Match      12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGGT 46
Db 2 TCCTTTAAGAGGT 14

RESULT 84
US-09-597-732-99
```

; Sequence 99, Application US/09597732
 ; Patent No. 6451534
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating, Mark T.
 ; APPLICANT: Sanguinetti, Michael C.
 ; APPLICANT: Curran, Mark E.
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Connors, Timothy D.
 ; APPLICANT: Burn, Timothy C.
 ; APPLICANT: Splawski, Igor
 ; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
 ; FILE REFERENCE: 2323-133
 ; CURRENT APPLICATION NUMBER: US/09/597,732
 ; CURRENT FILING DATE: 2000-06-19
 ; PRIOR APPLICATION NUMBER: 09/135,010
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 60/094,477
 ; PRIOR FILING DATE: 1998-07-29
 ; PRIOR APPLICATION NUMBER: 08/921,068
 ; PRIOR FILING DATE: 1997-08-29
 ; PRIOR APPLICATION NUMBER: 08/739,383
 ; PRIOR FILING DATE: 1996-10-29
 ; PRIOR APPLICATION NUMBER: 60/019,014
 ; PRIOR FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 99
 ; LENGTH: 14
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-597-732-99

Query Match 12.7%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 51;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 TCCTCTGAGAGGT 46
 |||||
 Db 2 TCCTTTAAGAGGT 14

RESULT 85
 US-09-597-731-99
 ; Sequence 99, Application US/09597731
 ; Patent No. 6582913
 ; GENERAL INFORMATION:
 ; APPLICANT: Keating, Mark T.
 ; APPLICANT: Sanguinetti, Michael C.
 ; APPLICANT: Curran, Mark E.
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Connors, Timothy D.
 ; APPLICANT: Burn, Timothy C.
 ; APPLICANT: Splawski, Igor
 ; TITLE OF INVENTION: KVLQT1 - A LONG QT SYNDROME GENE
 ; FILE REFERENCE: 2323-133
 ; CURRENT APPLICATION NUMBER: US/09/597,731
 ; CURRENT FILING DATE: 2000-06-19
 ; PRIOR APPLICATION NUMBER: 09/135,010
 ; PRIOR FILING DATE: 1998-08-17
 ; PRIOR APPLICATION NUMBER: 08/921,068
 ; PRIOR FILING DATE: 1997-08-29
 ; PRIOR APPLICATION NUMBER: 08/739,383
 ; PRIOR FILING DATE: 1996-10-29
 ; PRIOR APPLICATION NUMBER: 60/019,014
 ; PRIOR FILING DATE: 1995-12-22
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 99
 ; LENGTH: 14
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-597-731-99

Query Match 12.7%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 51;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 34 TCCTCTGAGAGGT 46
 |||||
 Db 2 TCCTTTAAGAGGT 14

RESULT 86
 US-09-401-063-1769
 ; Sequence 1769, Application US/09401063
 ; Patent No. 6623962
 ; GENERAL INFORMATION:
 ; APPLICANT: Akhtar, Saghir
 ; APPLICANT: Fell, Patricia
 ; APPLICANT: McSwiggen, James
 ; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
 ; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
 ; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
 ; TITLE OF INVENTION: FACTOR RECEPTORS
 ; NUMBER OF SEQUENCES: 1877
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: FastSeq for Windows 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/401,063
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/985,162
 ; FILING DATE: 04 December 1997
 ; APPLICATION NUMBER: 60/036,476
 ; FILING DATE: 31 January 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 230/107
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 1769:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-09-401-063-1769

Query Match 12.7%; Score 9.8; DB 1; Length 14;
 Best Local Similarity 84.6%; Pred. No. 51;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GACGGCTGGGGA 20
 |||||
 Db 2 GACGGCTGGGGA 14

RESULT 87
 PCT-US95-04712-26/c
 ; Sequence 26, Application PC/TUS9504712

GENERAL INFORMATION:
APPLICANT: Ligon, James M
APPLICANT: Beck, James J
TITLE OF INVENTION: Detection of Fungal Pathogens Using the
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04712
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,608
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Walsh, Andrea C.
REGISTRATION NUMBER: 34,988
REFERENCE/DOCKET NUMBER: CGC 1739
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8666
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: Oligonucleotide primer JB443
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-04712-26

Query Match 12.7%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 51;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCCTGGG 19
|||||
Db 13 AGACGGCCTCCG 1

RESULT 88
US-08-173-489C-331
Sequence 331, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT

OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 331:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: 16s rRNA gene from Neisseria
DESCRIPTION: gonorrhoeae (Accession # X07714) nucleotides
DESCRIPTION: 189 to 199
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Neisseria gonorrhoeae
STRAIN: NCTC 83785
PUBLICATION INFORMATION:
AUTHORS: Rossau, R. Heyndrickx, L. van
AUTHORS: Heuvelswyn, H.
TITLE: Nucleotide sequence of a 16s
TITLE: ribosomal RNA gene from Neisseria gonorrhoeae
JOURNAL: Nucleic Acids Research
VOLUME: 16
PAGES: 6227-6227
DATE: 1988
RELEVANT RESIDUES IN SEQ ID NO: 331 :FROM 1 TO 11
US-08-173-489C-331

Query Match 12.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 48;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 40 GAGAGGTAAG 50
|||||
Db 1 GAGAGGGAAAG 11

RESULT 89
US-09-940-244-415
Sequence 415, Application US/09940244
Patent No. 6692917
GENERAL INFORMATION:
APPLICANT: Neri, Bruce P.
APPLICANT: Hall, Jeff G.
APPLICANT: Lyamichev, Victor
APPLICANT: Smith, Lloyd M.
TITLE OF INVENTION: Reactions on Dendrimers
FILE REFERENCE: FORS-06478
CURRENT APPLICATION NUMBER: US/09/940,244
CURRENT FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PatentIn version 3.1
SEQ ID NO 415
LENGTH: 12
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic

FEATURE:
NAME/KEY: misc feature
LOCATION: (4)...(4)
OTHER INFORMATION: The residue at this position is linked to a spacer bearing a Cy3
OTHER INFORMATION: dye.
US-09-940-244-415

Query Match 12.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 52;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 31 GAGTCCTCTGA 41
Db 1 GAGTCCTGTGA 11

RESULT 90
US-08-738-944-39
Sequence 39, Application US/08738944
Patent No. 5783431
GENERAL INFORMATION:
APPLICANT: Peterson, et al.
TITLE OF INVENTION: METHODS FOR GENERATING AND
SCREENING NOVEL METABOLIC PATHWAYS
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,944
FILING DATE: 24-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/639,255
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8757-007
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Other
LOCATION: 5...6
OTHER INFORMATION: pDBLET Vector
US-08-738-944-39

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAA 60
Db 3 GAGCCAGCTAA 13

RESULT 91
US-08-468-037A-26/c
Sequence 26, Application US/08468037A
Patent No. 5859221
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: A. Kawasaki
TITLE OF INVENTION: 2'-Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859221ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,037A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 835,932
FILING DATE: 05-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Joseph Lucci
REGISTRATION NUMBER: 33,307
REFERENCE/DOCKET NUMBER: ISIS-2004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-468-037A-26

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGG 17
Db 12 AAACGGCCTGG 2

RESULT 92
US-08-471-973A-26/c
Sequence 26, Application US/08471973A
Patent No. 5872232
GENERAL INFORMATION:
APPLICANT: Phillip Dan Cook
APPLICANT: Andrew Kawasaki
TITLE OF INVENTION: Sugar Modified Oligonucleotides
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5872232ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720 Kb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,973A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 835,932
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-973A-26

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17
Db 12 AAACGGCCTGG 2

RESULT 93
US-09-035-357-26/c
; Sequence 26, Application US/09035357
; Patent No. 6005087
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6005087ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035,357
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/468,037
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
US-09-035-357-26

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCCTGG 17
Db 12 AAACGGCCTGG 2

RESULT 94
US-09-263-352-30
; Sequence 30, Application US/09263352
; Patent No. 6242211
; GENERAL INFORMATION:
; APPLICANT: Brian, P.
; APPLICANT: Peterson, T.
; TITLE OF INVENTION: METHODS FOR GENERATING AND SCREENING NOVEL METABOLIC
; FILE REFERENCE: 8757-010
; CURRENT APPLICATION NUMBER: US/09/263,352
; CURRENT FILING DATE: 1999-03-05
; EARLIER APPLICATION NUMBER: 08/986,186
; EARLIER FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: linker
; US-09-263-352-30

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAA 60
Db 3 GAGCCAGCTAA 13

RESULT 95
US-08-936-166-6/c
; Sequence 6, Application US/08936166A
; Patent No. 6307040
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Sugar Modified Oligonucleotides That Detect And
; FILE REFERENCE: ISIS2708
; CURRENT APPLICATION NUMBER: US/08/936,166A
; CURRENT FILING DATE: 1997-09-23
; EARLIER APPLICATION NUMBER: 07/835,932
; EARLIER FILING DATE: 1992-03-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleoside
; OTHER INFORMATION: having a modified sugar moiety
; US-08-936-166-6

Query Match 12.2%; Score 9.4; DB 1; Length 13;
```


Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGG 17

Db 12 AAACGGCCTGG 2

RESULT 96

US-09-135-202-26/c
; Sequence 26, Application US/09135202
; Patent No. 6399754
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6399754ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA: US/09/135,202
; APPLICATION NUMBER: US/09/135,202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-135-202-26

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 AGACGGCCTGG 17

Db 12 AAACGGCCTGG 2

RESULT 97

US-09-474-432B-141
; Sequence 141, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn

; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 141
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-474-432B-141

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAAGAGCCAGC 57

Db 2 AGAGAGCCAGC 12

RESULT 98

US-09-389-283-26/c
; Sequence 26, Application US/09389283
; Patent No. 6531584
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; APPLICANT: A. Kawasaki
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6531584ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/389,283
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/035,357
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-389-283-26

Query Match 12.2%; Score 9.4; DB 1; Length 13;

```
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AGACGGCTGG 17
Db 12 AAACGGCTGG 2

RESULT 99
US-09-476-387-141
; Sequence 141, Application US/09476387
; Patent No. 6617438
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MHB00-831-C (249/073)
; CURRENT APPLICATION NUMBER: US/09/476,387
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1524
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 141
; LENGTH: 13
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-476-387-141

Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGC 57
Db 2 AGAGAGCCAGC 12

RESULT 100
US-10-042-819-8/c
; Sequence 8, Application US/10042819
; Patent No. 6897025
; GENERAL INFORMATION:
; APPLICANT: Perlegen Sciences, Inc.
; APPLICANT: Cox, David R
; APPLICANT: Margus, Bradley A
; TITLE OF INVENTION: GENETIC ANALYSIS SYSTEM AND METHODS
; FILE REFERENCE: 1016N1
; CURRENT APPLICATION NUMBER: US/10/042,819
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL SEQUENCE
US-10-042-819-8
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Query Match 12.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 46 TAAAGAGCCAG 56
Db 12 TAAAGAGTCAG 2

Search completed: April 19, 2006, 16:10:20
Job time : 0.001 secs
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DR WPI; 2003-140495/13.
XX
PT New compound that hybridizes with and inhibits the expression of
PT Phospholipase A2, group IIA, useful for preparing a composition for
PT treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
XX Claim 3; Page 86; 135pp; English.
XX
XX The present invention describes a compound (I) comprising 8-50
CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
CC A2, group IIA (synovial), where the compound specifically hybridizes with
CC and inhibits the expression of phospholipase A2, group IIA (synovial).
CC Also described: (1) a composition comprising the compound and a carrier
CC or diluent; (2) a method of inhibiting the expression of phospholipase
CC A2, group IIA in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with phospholipase A2, group IIA
CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
CC antipsoriatic activities, and can be used in vaccines and in gene
CC therapy. The compound (I) can be used for preparing a composition for
CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
CC present sequence represents a human phospholipase A2 group IIA (synovial)
CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
CC example from the present invention
XX
SQ Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CTCGAGAGGTAAGAGCCA 55
DB 20 CTCGAGAGGTAAGAGCCA 1

RESULT 7
ACC46925/c
ID ACC46925 standard; DNA; 20 BP.
XX
AC ACC46925;
XX
XX 05-JUN-2003 (first entry)
XX
DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:22.
XX
KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
KW psoriasis; diabetes; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
PN WO200297133-A1.
XX
PD 05-DEC-2002.
XX
PP 21-MAY-2002; 2002WO-US016135.

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XX 25-MAY-2001; 2001US-00865866.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Wyatt JR;
XX WPI; 2003-140495/13.
XX
XX New compound that hybridizes with and inhibits the expression of
XX Phospholipase A2, group IIA, useful for preparing a composition for
XX treating or preventing inflammation, cancer, psoriasis or diabetes.
XX Claim 3; Page 86; 135pp; English.
XX
XX The present invention describes a compound (I) comprising 8-50
CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
CC A2, group IIA (synovial), where the compound specifically hybridizes with
CC and inhibits the expression of phospholipase A2, group IIA (synovial).
CC Also described: (1) a composition comprising the compound and a carrier
CC or diluent; (2) a method of inhibiting the expression of phospholipase
CC A2, group IIA in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with phospholipase A2, group IIA
CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
CC antipsoriatic activities, and can be used in vaccines and in gene
CC therapy. The compound (I) can be used for preparing a composition for
CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
CC present sequence represents a human phospholipase A2 group IIA (synovial)
CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
CC example from the present invention
XX
SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTCCTCTGAGAGGTAAGAG 52
DB 20 GTCCTCTGAGAGGTAAGAG 1

RESULT 8
ACC46922/c
ID ACC46922 standard; DNA; 20 BP.
XX
AC ACC46922;
XX
XX 05-JUN-2003 (first entry)
XX
DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:19.
XX
KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
KW psoriasis; diabetes; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER

```

CC or diluent; (2) a method of inhibiting the expression of phospholipase
 CC A2, group IIA in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with phospholipase A2, group IIA
 CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
 CC antipsoriatic activities, and can be used in vaccines and in gene
 CC therapy. The compound (I) can be used for preparing a composition for
 CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
 CC present sequence represents a human phospholipase A2 group IIA (synovial)
 CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
 CC example from the present invention

XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 26.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 GAAGCTGATGTCCTGTCAG 77
 |||||
 Db 20 GAAGCTGATGTCCTGTCAG 1

RESULT 5
 ACC46927/c
 ID ACC46927 standard; DNA; 20 BP.

XX ACC46927;

XX 05-JUN-2003 (first entry)

DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:24.

XX Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
 KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
 KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
 KW psoriasis; diabetes; ss.

OS Homo sapiens.
 OS Synthetic.

Key	Location/Qualifiers
modified_base	1..20
	/*tag= a
	/mod_base= OTHER
	/note= "phosphorothioate backbone"
modified_base	1..5
	/*tag= b
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) gapmer"
modified_base	16..20
	/*tag= c
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) gapmer"

WO200297133-A1.

XX 05-DEC-2002.

XX 21-MAY-2002; 2002WO-US016135.

XX 25-MAY-2001; 2001US-00865866.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

XX WPI; 2003-140495/13.

XX New compound that hybridizes with and inhibits the expression of
 PT Phospholipase A2, group IIA, useful for preparing a composition for
 PT treating or preventing inflammation, cancer, psoriasis or diabetes.

XX Example 15; Page 86; 135pp; English.

XX The present invention describes a compound (I) comprising 8-50
 CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
 CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
 CC A2, group IIA (synovial), where the compound specifically hybridizes with
 CC and inhibits the expression of phospholipase A2, group IIA (synovial).
 CC Also described: (1) a composition comprising the compound and a carrier
 CC or diluent; (2) a method of inhibiting the expression of phospholipase
 CC A2, group IIA in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with phospholipase A2, group IIA
 CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
 CC antipsoriatic activities, and can be used in vaccines and in gene
 CC therapy. The compound (I) can be used for preparing a composition for
 CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
 CC present sequence represents a human phospholipase A2 group IIA (synovial)
 CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
 CC example from the present invention

XX Sequence 20 BP; 1 A; 7 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 26.0%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AGAGGTAAGAGCCAGCGAA 60
 |||||
 Db 20 AGAGGTAAGAGCCAGCGAA 1

RESULT 6
 ACC46926/c

ID ACC46926 standard; DNA; 20 BP.

XX ACC46926;

XX 05-JUN-2003 (first entry)

DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:23.

XX Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
 KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
 KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
 KW psoriasis; diabetes; ss.

OS Homo sapiens.
 OS Synthetic.

Key	Location/Qualifiers
modified_base	1..20
	/*tag= a
	/mod_base= OTHER
	/note= "phosphorothioate backbone"
modified_base	1..5
	/*tag= b
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) gapmer"
modified_base	16..20
	/*tag= c
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) gapmer"

WO200297133-A1.

XX 05-DEC-2002.

XX 21-MAY-2002; 2002WO-US016135.

XX 25-MAY-2001; 2001US-00865866.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

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FT      /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
PN      WO200297133-A1.
XX
XX      05-DEC-2002.
XX
XX      21-MAY-2002; 2002WO-US016135.
XX
XX      25-MAY-2001; 2001US-00865866.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Bennett CF, Wyatt JR;
XX      WPI; 2003-140495/13.
XX
XX      New compound that hybridizes with and inhibits the expression of
XX      phospholipase A2, group IIA, useful for preparing a composition for
XX      treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
XX      Claim 3; Page 86; 135pp; English.
XX
XX      The present invention describes a compound (I) comprising 8-50
XX      nucleobases which is targeted to a 5' untranslated region (UTR), coding,
XX      3' UTR or intron region of a nucleic acid molecule encoding phospholipase
XX      A2, group IIA (synovial), where the compound specifically hybridizes with
XX      and inhibits the expression of phospholipase A2, group IIA (synovial).
XX      Also described: (1) a composition comprising the compound and a carrier
XX      or diluent; (2) a method of inhibiting the expression of phospholipase
XX      A2, group IIA in cells or tissues; and (3) a method of treating an animal
XX      having a disease or condition associated with phospholipase A2, group IIA
XX      (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
XX      antipsoriatic activities, and can be used in vaccines and in gene
XX      therapy. The compound (I) can be used for preparing a composition for
XX      treating or preventing inflammation, cancer, psoriasis or diabetes. The
XX      present sequence represents a human phospholipase A2 group IIA (synovial)
XX      chimeric phosphorothioate antisense oligonucleotide, which is used in an
XX      example from the present invention
XX
XX      Sequence 20 BP; 1 A; 7 C; 5 G; 7 T; 0 U; 0 Other;
XX
XX      Query Match      26.0%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 6.7;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 CAAACAGACGGCTGGGA 20
DB      |||||
        20 CAAACAGACGGCTGGGA 1

RESULT 9
ACC46924/c
ID      ACC46924 standard; DNA; 20 BP.
XX
XX      ACC46924;
XX
XX      05-JUN-2003 (first entry)
XX
XX      Human phospholipase A2 antisense oligonucleotide SEQ ID NO:21.
XX
XX      Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
XX      phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
XX      antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
XX      psoriasis; diabetes; ss.
XX
XX      Homo sapiens.
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      modified_base 1..20
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "phosphorothioate backbone"

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FT      modified_base 1..5
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT      modified_base 16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX
XX      WO200297133-A1.
XX
XX      05-DEC-2002.
XX
XX      21-MAY-2002; 2002WO-US016135.
XX
XX      25-MAY-2001; 2001US-00865866.
XX
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Bennett CF, Wyatt JR;
XX      WPI; 2003-140495/13.
XX
XX      New compound that hybridizes with and inhibits the expression of
XX      phospholipase A2, group IIA, useful for preparing a composition for
XX      treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
XX      Claim 3; Page 86; 135pp; English.
XX
XX      The present invention describes a compound (I) comprising 8-50
XX      nucleobases which is targeted to a 5' untranslated region (UTR), coding,
XX      3' UTR or intron region of a nucleic acid molecule encoding phospholipase
XX      A2, group IIA (synovial), where the compound specifically hybridizes with
XX      and inhibits the expression of phospholipase A2, group IIA (synovial).
XX      Also described: (1) a composition comprising the compound and a carrier
XX      or diluent; (2) a method of inhibiting the expression of phospholipase
XX      A2, group IIA in cells or tissues; and (3) a method of treating an animal
XX      having a disease or condition associated with phospholipase A2, group IIA
XX      (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
XX      antipsoriatic activities, and can be used in vaccines and in gene
XX      therapy. The compound (I) can be used for preparing a composition for
XX      treating or preventing inflammation, cancer, psoriasis or diabetes. The
XX      present sequence represents a human phospholipase A2 group IIA (synovial)
XX      chimeric phosphorothioate antisense oligonucleotide, which is used in an
XX      example from the present invention
XX
XX      Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX      Query Match      26.0%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 6.7;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      23 CAACTCTGGAGTCTCTGAG 42
DB      |||||
        20 CAACTCTGGAGTCTCTGAG 1

RESULT 10
ACC46923/c
ID      ACC46923 standard; DNA; 20 BP.
XX
XX      ACC46923;
XX
XX      05-JUN-2003 (first entry)
XX
XX      Human phospholipase A2 antisense oligonucleotide SEQ ID NO:20.
XX
XX      Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
XX      phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
XX      antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
XX      psoriasis; diabetes; ss.
XX
XX      Homo sapiens.

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OS Synthetic.
XX Key Location/Qualifiers
PH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /*note= "phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /*note= "2'-O-methoxyethyl (2'-MOE) gapmer"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /*note= "2'-O-methoxyethyl (2'-MOE) gapmer"
XX WO200297133-A1.
PN XX
PD XX
PD 05-DEC-2002.
XX
XX 21-MAY-2002; 2002WO-US016135.
XX
XX 25-MAY-2001; 2001US-00865866.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Wyatt JR;
XX WPI; 2003-140495/13.
XX
XX New compound that hybridizes with and inhibits the expression of
XX phospholipase A2, group IIA, useful for preparing a composition for
XX treating or preventing inflammation, cancer, psoriasis or diabetes.
XX
XX Claim 3; Page 86; 135pp; English.
XX
XX The present invention describes a compound (I) comprising 8-50
XX nucleobases which is targeted to a 5' untranslated region (UTR), coding,
XX 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
XX A2, group IIA (synovial), where the compound specifically hybridises with
XX and inhibits the expression of phospholipase A2, group IIA (synovial).
XX Also described: (1) a composition comprising the compound and a carrier
XX or diluent; (2) a method of inhibiting the expression of phospholipase
XX A2, group IIA in cells or tissues; and (3) a method of treating an animal
XX having a disease or condition associated with phospholipase A2, group IIA
XX (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
XX antiproliferative activities, and can be used in vaccines and in gene
XX therapy. The compound (I) can be used for preparing a composition for
XX treating or preventing inflammation, cancer, psoriasis or diabetes. The
XX present sequence represents a human phospholipase A2 group IIA (synovial)
XX chimeric phosphorothioate antisense oligonucleotide, which is used in an
XX example from the present invention
XX
SQ Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 26.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GCCTGGGGATACAACTCTGG 31
DB 20 GCCTGGGGATACAACTCTGG 1

RESULT 11
ID ACL45000/c
XX ACL45000 standard; RNA; 21 BP.
XX
XX ACL45000;
XX
XX 24-MAR-2005 (first entry)
XX
XX CDH6 siRNA antisense sequence, SEQ ID 6072.

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XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX short interfering RNA; gene silencing.
XX Synthetic.
XX WO2005001092-A2.
XX
PD 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 6072; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 3 A; 6 C; 5 G; 0 T; 7 U; 0 Other;

Query Match 23.1%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 AAGAGCCAGCGAGCTGATGT 68
DB 21 AAGAGCCAGCGAGCTGATGT 1

RESULT 12
ID ACL44998
XX ACL44998 standard; DNA; 21 BP.
XX
XX ACL44998;
XX
XX 24-MAR-2005 (first entry)
XX
XX CDH6 target oligonucleotide, SEQ ID 6070.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX

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Query Match 21.3%; Score 16.4; DB 1; Length 21;
 Best Local Similarity 94.4%; Pred. No. 27;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 AGCCAGCGAGCTGATGT 68
 |||||
 DB 2 AGCCAGCGAGCTGATGT 19

RESULT 17
 ACL4499/c
 ID ACL4499 standard; RNA; 21 BP.
 AC ACL4499;
 XX
 XX 24-MAR-2005 (first entry)
 XX
 XX CDH6 siRNA antisense sequence, SEQ ID 5571.
 DE
 XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
 KW short interfering RNA; gene silencing.
 KW
 XX Synthetic.
 OS
 XX WO2005001092-A2.
 PN
 XX 06-JAN-2005.
 PD
 XX 19-MAY-2004; 2004WO-US015645.
 PP
 XX 20-MAY-2003; 2003US-0471729P.
 PR
 XX (AMHP) WYETH.
 PA
 XX Be X, Wei L, Slonim DK, Howes SH;
 PI
 XX WPI; 2005-075568/08.
 DR
 XX Pharmaceutical composition comprising an agent capable of modulating an
 PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell
 PT activated by the polypeptide or antibody, and a carrier, useful for
 PT treating cancer.
 PT
 XX Claim 3; SEQ ID NO 5571; 113pp; English.
 PS
 XX The present invention relates to a novel pharmaceutical composition
 CC comprising: (a) an agent capable of modulating an expression level or
 CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
 CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
 CC (b) a carrier. The pharmaceutical composition may also comprise a
 CC polynucleotide capable of inhibiting or decreasing the expression of the
 CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
 CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
 CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
 CC pharmaceutical composition is useful for treating cancer, e.g. colon
 CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
 CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
 CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 21 BP; 3 A; 8 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 21.3%; Score 16.4; DB 1; Length 21;
 Best Local Similarity 94.4%; Pred. No. 27;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 51 AGCCAGCGAGCTGATGT 68
 |||||
 DB 20 AGCCAGCGAGCTGATGT 3

RESULT 18
 ACL44999
 ID ACL44999 standard; RNA; 21 BP.
 XX
 AC ACL44999;
 XX
 XX 24-MAR-2005 (first entry)
 DT
 XX CDH6 siRNA sense sequence, SEQ ID 6071.
 XX
 XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
 KW short interfering RNA; gene silencing.
 KW
 XX Synthetic.
 OS
 XX WO2005001092-A2.
 PN
 XX 06-JAN-2005.
 PD
 XX 19-MAY-2004; 2004WO-US015645.
 PP
 XX 20-MAY-2003; 2003US-0471729P.
 PR
 XX (AMHP) WYETH.
 PA
 XX Be X, Wei L, Slonim DK, Howes SH;
 PI
 XX WPI; 2005-075568/08.
 DR
 XX Pharmaceutical composition comprising an agent capable of modulating an
 PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell
 PT activated by the polypeptide or antibody, and a carrier, useful for
 PT treating cancer.
 PT
 XX Claim 3; SEQ ID NO 6071; 113pp; English.
 PS
 XX The present invention relates to a novel pharmaceutical composition
 CC comprising: (a) an agent capable of modulating an expression level or
 CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
 CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
 CC (b) a carrier. The pharmaceutical composition may also comprise a
 CC polynucleotide capable of inhibiting or decreasing the expression of the
 CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
 CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
 CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
 CC pharmaceutical composition is useful for treating cancer, e.g. colon
 CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
 CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
 CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX Sequence 21 BP; 5 A; 5 C; 6 G; 0 T; 5 U; 0 Other;

Query Match 21.3%; Score 16.4; DB 1; Length 21;
 Best Local Similarity 77.8%; Pred. No. 27;
 Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 51 AGCCAGCGAGCTGATGT 68
 |||||
 DB 2 AGCCAGCGAGCTGATGT 19

RESULT 19
 AAT4824/c
 ID AAT4824 standard; DNA; 20 BP.
 XX
 AC AAT4824;
 XX
 XX 16-SEP-1997 (first entry)
 DT
 XX

DE PLA2s exon 1 primer, AB4.
 XX Polymerase chain reaction; PCR; amplify; primer; PLA2s; mutation; APC;
 KW type II non-pancreatic phospholipase A2; microsatellite; colon cancer;
 KW adenomatous polyposis coli; ss.
 XX Synthetic.
 XX WO9641003-A1.
 XX 19-DEC-1996.
 XX 06-JUN-1996; 96WO-US009009.
 XX 07-JUN-1995; 95US-00484359.
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX Buchberg AM, Siracusa LD, Chepenik KP;
 PI WPI; 1997-052369/05.
 DR Identifying an individual at an elevated risk of colon cancer - by
 XX detecting mutation(s) in PLA2s gene.
 XX Example 1; Page 16; 78pp; English.
 XX The sequences given in AAT48821-34 are primers which were used to amplify
 CC regions of the type II non-pancreatic phospholipase A2 (PLA2s) gene at
 CC which mutations occur. These primers amplify regions upstream of the
 CC first exon and exon one, around the microsatellite, and exons 2, 3, 4 and
 CC 5 and the surrounding sequences. These primers may be used in the method
 CC of the invention for identifying an individual at an elevated risk of
 CC colon cancer. The method comprises: (a) isolating genetic material from a
 CC tissue or body fluid sample from the individual; and (b) detecting a
 CC PLA2s gene mutation which is indicative of the individual is at an
 CC elevated risk of colon cancer; or (b') detecting the absence of PLA2s
 CC protein or PLA2s enzyme activity in an isolated protein sample which is
 CC indicative of the individual having an elevated risk of colon cancer. The
 CC method allows individuals with the APC (adenomatous polyposis coli)
 CC mutation to be identified. In the treatment of colon cancer, the patient
 CC is administered a recombinant vector incorporated within a non-toxic
 CC enteric microorganism which expresses and secretes PLA2s
 XX
 SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 20.8%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 62 CTGATGTCCTGTCAG 77
 Db 20 CTGATGTCCTGTCAG 5
 RESULT 20
 AD297584
 ID AD297584 standard; DNA; 21 BP.
 XX AD297584;
 AC AD297584;
 DT 14-JUL-2005 (first entry)
 XX Canine SNP detection, forward PCR primer SEQ ID No:181.
 DE animal breeding; genetic marker; SNP detection; allelic variation;
 KW infection; diabetes; hypertension; atherosclerosis; autoimmune disease;
 KW renal disease; neurological disease; PCR; primer; ss.
 XX Canidae.
 OS WO2005040350-A2.
 XX
 PN

PD 06-MAY-2005.
 XX 25-OCT-2004; 2004WO-US035231.
 XX 24-OCT-2003; 2003US-0514180P.
 PR 08-OCT-2004; 2004US-0617383P.
 XX (MMIG-) MMI GENOMICS INC.
 PA Rosenfeld D, Kerr R, Hutton M, Denise S, Bates S, Fantin D;
 PI WPI; 2005-333502/34.
 DR Identifying animal genetic marker that influences trait for determining
 XX parentage or to infer breed/line in e.g. canines involves analyzing
 PT markers of genome-wide genetic marker map for association with genetic
 PT trait.
 XX Claim 44; SEQ ID NO 181; 145pp; English.
 PS The invention relates to a method of identifying a companion animal
 XX genetic marker that influences a phenotype or trait comprising analyzing
 CC companion animal genetic markers of a genome-wide genetic marker map for
 CC association with the genetic trait and identifying the companion animal
 CC genetic marker that influences the trait. Also described are: (i) a high
 CC throughput system for determining the nucleotide occurrences at a series
 CC of companion animal SNPs comprising a hybridization medium containing a
 CC series of oligonucleotides that bind at or near a genomic location of
 CC each SNP of the series of companion animal SNPs, a mechanism for moving
 CC the solid support or other hybridization medium, and a liquid handling
 CC mechanism for applying a liquid to the series of oligonucleotides,
 CC binding of oligonucleotide to a polynucleotide isolated from a genome is
 CC affected by the nucleotide occurrence of the SNP; (ii) a kit for
 CC determining nucleotide occurrences of canine SNPs, comprising an
 CC oligonucleotide probe and/or primer/primer pair for identifying the
 CC nucleotide occurrence of at least one canine SNP corresponding to the
 CC first nucleotide or complement in the most 3' position of nucleotide
 CC sequences given as SEQ ID Nos 1-101 in the specification; (iii) a
 CC database comprising each SNP corresponding to the first nucleotide or
 CC complement in the most 3' position of nucleotide sequences in SEQ ID Nos
 CC 1-101; (iv) a computer-based method for identifying/infering a trait of
 CC a canine test involving identifying from the obtained subject nucleic
 CC acid sample at least one nucleotide occurrence of at least one SNP
 CC corresponding to the first nucleotide, or complement its in the most 3'
 CC position of nucleotide sequences in SEQ ID Nos 1-101, searching a
 CC database comprising allele frequencies and retrieving information,
 CC optionally storing the information in a memory location associated with a
 CC user such that the information may be subsequently accessed and viewed by
 CC the user, and identifying the trait of a canine subject; (v) an isolated
 CC oligonucleotide comprising any one of the nucleotide sequences given as
 CC SEQ ID Nos 306-407 in the specification, and further including one
 CC additional nucleotide positioned proximal to the 3' end of each
 CC oligonucleotide that specifically hybridizes to a nucleic acid sequence
 CC derived from a canine subject, or a first nucleotide or its complement
 CC with nucleotide sequences in SEQ ID Nos 1-101; (vi) an isolated SNP
 CC corresponding to the first nucleotide or complement in the most 3'
 CC position of any one of the nucleotide sequences in SEQ ID Nos 1-101;
 CC (vii) a panel comprising at least one SNP corresponding to the first
 CC nucleotide, or complement in the most 3' position of a nucleotide
 CC sequence in SEQ ID Nos 1-101; (viii) generating a genome discovery map
 CC involving selecting several SNP markers corresponding to the first
 CC nucleotide or complement in the most 3' position of any one of nucleotide
 CC sequence in SEQ ID Nos 1-101, each marker in the series separated by
 CC 150000 bp, and generating the genome discovery map based upon the
 CC selected markers; (ix) identifying the parentage of a canine test subject
 CC involving obtaining a nucleic acid sample from the test subject by
 CC identifying in the nucleic acid sample at least one SNP corresponding to
 CC the first nucleotide or complement in the most 3' position of any one of
 CC nucleotide sequence in SEQ ID Nos 1-101, determining the alleles to
 CC corresponding to each SNP identified, and comparing the alleles to
 CC putative parents of the test subject such that parents that do not
 CC possess at least one allele in common with the test subject are excluded,
 CC and (x) the use of a first primer selected from SEQ ID Nos 102-203, and a

CC second primer selected from SEQ ID Nos 204-305 in the method of the
 CC invention. The method is useful for identifying a companion animal
 CC genetic marker that influences a phenotype or trait and determine the
 CC parentage or to infer breed/line of a canine test subject, for
 CC identifying/infering a genetic trait (preferably resistant to disease or
 CC infection), susceptibility to infection, regulation of immune status and
 CC response to antigens, previous exposure to infection or parasites,
 CC bone/joint health, coat color/health, body mass, health of respiratory
 CC and digestive tissues, diabetes, hypertension, atherosclerosis,
 CC autoimmune disorders, kidney disease and neurological disease in
 CC companion animal (preferably dogs, cats, fish, reptiles, birds, horses,
 CC rabbits, hamsters, gerbils, mice or rats, especially dog). The
 CC methods/systems help for managing, selecting and breeding companion
 CC animals, maximizing individual potential performance and health, allowing
 CC predictive (predisposition) diagnostics, nutritional therapies and
 CC veterinary pharmaceutical therapeutics as applied to companion animals,
 CC and collect, record and store data by individual animal identification so
 CC that it is usable to improve future animals bred by animal owners and
 CC breeders. The methods/systems are also useful for assessing complex
 CC traits such as energy metabolism, aging and breed-specific traits to
 CC improve profits related to selling a companion animal, to manage, sort,
 CC and improve the genetics of a companion animal population by selecting
 CC and breeding of companion animal, to clone a companion animal with a
 CC specific genetic trait(s) or combination of SNP markers that predict a
 CC genetic trait, to track a companion animal or offspring, and to diagnose
 CC a health condition of a companion animal. This sequence represents a PCR
 CC primer used for the detection of canine SNPs.

XX
 SQ Sequence 21 BP; 6 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 20.5%; Score 15.8; DB 1; Length 21;
 Best Local Similarity 89.5%; Pred. No. 33;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 39 TGAGAGCTTAAGGCCAGC 57
 Db 1 TGAGTGGTAATAGCCAGC 19

RESULT 21
 ACL44498
 ID ACL44498 standard; RNA; 21 BP.
 AC ACL44498;
 XX
 XX 24-MAR-2005 (first entry)
 XX
 DE CDH6 siRNA sense sequence, SEQ ID 5570.
 XX
 XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
 KW short interfering RNA; gene silencing.
 XX
 XX Synthetic.
 XX
 XX W02005001092-A2.
 PN
 XX
 PD 06-JAN-2005.
 XX
 XX 19-MAY-2004; 2004WO-US015645.
 XX
 XX 20-MAY-2003; 2003US-0471729P.
 PR
 XX
 XX (AMHP) WYETH.
 PA

PI Be X, Wei L, Slonim DK, Howes SH;
 XX
 XX WPI; 2005-075568/08.
 DR
 XX
 XX Pharmaceutical composition comprising an agent capable of modulating an
 PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
 PT activated by the polypeptide or antibody, and a carrier, useful for
 PT treating cancer.
 XX

PS Claim 3; SEQ ID NO 5570; 113pp; English.

XX The present invention relates to a novel pharmaceutical composition
 CC comprising: (a) an agent capable of modulating an expression level or
 CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
 CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
 CC (b) a carrier. The pharmaceutical composition may also comprise a
 CC polynucleotide capable of inhibiting or decreasing the expression of the
 CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
 CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
 CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
 CC pharmaceutical composition is useful for treating cancer, e.g. colon
 CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
 CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
 CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences

XX
 SQ Sequence 21 BP; 3 A; 5 C; 8 G; 0 T; 5 U; 0 Other;

Query Match 20.0%; Score 15.4; DB 1; Length 21;
 Best Local Similarity 76.5%; Pred. No. 38;
 Matches 13; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 52 GCCAGCGAAGCTGATGT 68
 Db 1 GCCAGCGAGCGUGAUGU 17

RESULT 22
 ADD35279
 ID ADD35279 standard; DNA; 22 BP.
 XX
 AC ADD35279;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Human KIAA0172 exon 1 primer #14.
 XX
 KW human; KIAA0172; cancer; ss; PCR; primer.
 XX
 OS Homo sapiens.
 XX
 PN JP2002369696-A.
 PD 24-DEC-2002.
 XX
 PF 01-APR-2002; 2002JP-00099422.
 XX
 XX 30-MAR-2001; 2001JP-00101401.
 PR
 XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
 PA (INFO-) INFO GENES CO LTD.
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
 XX
 XX WPI; 2003-495749/47.
 XX

PT Human KIAA0172 gene encoding a sequence of 1194 amino acids, useful for
 PT diagnosis and treatment of cancer and for development of effective growth
 PT inhibitors of cancer cells.
 XX
 XX Example 2; SEQ ID NO 15; 40pp; Japanese.
 PS
 XX The invention relates to new human KIAA0172 gene. The KIAA0172 gene and
 CC polypeptide are useful for detection and treatment of cancer. The present
 CC sequence represents KIAA0172 associated primer.

SQ Sequence 22 BP; 5 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 20.0%; Score 15.4; DB 1; Length 22;
 Best Local Similarity 94.1%; Pred. No. 40;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      60 AGCTGATGTCCTGTCAA 76
DB      2 AGCTGATGCGCTGTCAA 18

RESULT 23
ADK72854/c
ID      ADK72854 standard; DNA; 20 BP.
XX
AC      ADK72854;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Chimeric phosphorothioate oligonucleotide to target Nav1.3 #188.
XX
KW      Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW      diabetic neuropathy; arthritic pain; migraine headache;
KW      infantile epilepsy; ataxia; ss.
XX
OS      Synthetic.
XX
PN      WO2004016754-A2.
XX
PD      26-FEB-2004.
XX
PF      14-AUG-2003; 2003WO-US025465.
XX
PR      14-AUG-2002; 2002US-0403416P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Roberds SL;
XX
DR      WPI; 2004-203785/19.
XX
PT      New antisense compound targeted to a nucleic acid molecule encoding
PT      Nav1.3, useful for treating a disease or condition associated
PT      with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT      disorder, or ataxia.
XX
PS      Claim 4; SEQ ID NO 188; 417pp; English.
XX
CC      The present invention relates to an antisense compound targeted to a
CC      nucleic acid molecule encoding Nav1.3, where the antisense compound
CC      specifically hybridizes with and inhibits the expression of Nav1.3. The
CC      compound and composition are useful for treating a disease or condition
CC      associated with Nav1.3, e.g. pain including but not limited to
CC      neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC      diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC      pain from burns, migraine headache, cluster headache, mild-to-moderate
CC      headache; seizure disorder such as childhood seizure disorder, including
CC      but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC      sequence represents a chimeric phosphorothioate oligonucleotide with
CC      2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC      human Nav1.3 expression, the oligonucleotides are designed to target
CC      different regions of the human Nav1.3 RNA.
XX
SQ      Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match      19.7%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      34 TCCTCTGAGAGGTTAAAGAGC 53
DB      20 TCCTCTGAGGCAAGAGC 1

RESULT 24
ADK72874/c
ID      ADK72874 standard; DNA; 20 BP.
XX
AC      ADK72874;
XX
DT      20-MAY-2004 (first entry)
XX
DE      Chimeric phosphorothioate oligonucleotide to target Nav1.3 #208.
XX
KW      Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW      diabetic neuropathy; arthritic pain; migraine headache;
KW      infantile epilepsy; ataxia; ss.
XX
OS      Synthetic.
XX
PN      WO2004016754-A2.
XX
PD      26-FEB-2004.
XX
PF      14-AUG-2003; 2003WO-US025465.
XX
PR      14-AUG-2002; 2002US-0403416P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Roberds SL;
XX
DR      WPI; 2004-203785/19.
XX
PT      New antisense compound targeted to a nucleic acid molecule encoding
PT      Nav1.3, useful for treating a disease or condition associated
PT      with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT      disorder, or ataxia.
XX
PS      Claim 4; SEQ ID NO 208; 417pp; English.
XX
CC      The present invention relates to an antisense compound targeted to a
CC      nucleic acid molecule encoding Nav1.3, where the antisense compound
CC      specifically hybridizes with and inhibits the expression of Nav1.3. The
CC      compound and composition are useful for treating a disease or condition
CC      associated with Nav1.3, e.g. pain including but not limited to
CC      neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC      diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC      pain from burns, migraine headache, cluster headache, mild-to-moderate
CC      headache; seizure disorder such as childhood seizure disorder, including
CC      but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC      sequence represents a chimeric phosphorothioate oligonucleotide with
CC      2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC      human Nav1.3 expression, the oligonucleotides are designed to target
CC      different regions of the human Nav1.3 RNA.
XX
SQ      Sequence 20 BP; 2 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match      19.7%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      35 CCTCTGAGAGGTTAAAGAGCC 54
DB      20 CCTCTGAGGCAAGAGCC 1

RESULT 25
ABL44489/c
ID      ABL44489 standard; DNA; 20 BP.
XX
AC      ABL44489;
XX
DT      11-APR-2002 (first entry)
XX
DE      Human chromosome 1p36-35 PCR primer SEQ ID NO:1533.
XX
KW      Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
KW      PCR primer; ss.
XX
OS      Homo sapiens.

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XX JN2001321190-A.
 XX 20-NOV-2001.
 XX 12-MAR-2001; 2001JP-00068285.
 XX 10-MAR-2000; 2000JP-00066716.
 XX (RIKA) RIKAGAKU KENKYUSHO.
 XX (GENO-) GENOTEX YG.
 XX WPI; 2002-144136/19.
 XX Arraying genome clones.
 XX Claim 4; Page 35; 528pp; Japanese.
 XX The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multiwell plates numbered for discrimination are mixed in each of the
 CC multiwell plates; (b) a primer designed based on the chromosome marker
 CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multiwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multiwell
 CC plates; (e) the clones in the multiwell plates of the specified
 CC discrimination Nos. are mixed respectively in each wells of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstructed as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention
 XX
 SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 19.2%; Score 14.8; DB 1; Length 20;
 Best Local Similarity 88.9%; Pred. No. 44;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 46 TAAAGAGCCAGCGAGCT 63
 DB 18 TGAAGAGCCAGCGAGCT 1
 RESULT 26
 AAD35822
 ID AAD35822 standard; DNA; 21 BP.
 XX AAD35822;
 XX 26-JUL-2002 (first entry)
 XX RACE PCR primer #1, used for cloning human SU(FU) homologue.
 XX Human; Drosophila suppressor; human hedgehog-patched pathway; HH-PTC;
 KW sonic hedgehog-patched pathway; SHH-PTC; intracellular signal;
 KW split hand; split foot malformation type 3; SHFM3; wound healing;
 KW neurodegenerative disease; testicular; cancer; gene therapy; cytostatic;
 KW neuroprotective; rapid amplification of cDNA end; RACE; PCR; primer; ss.
 XX Homo sapiens.
 XX WO9932517-A1.
 XX 01-JUL-1999.
 XX

PF 18-DEC-1998; 98WO-SE002383.
 XX 19-DEC-1997; 97SE-00004788.
 PR 26-JUN-1998; 98SE-00002293.
 XX (KARO-) KAROLINSKA INNOVATIONS AB.
 XX Toftgard R, Zaphiropoulos PG, Kogerman P, Grimm T;
 PI WPI; 1999-405160/34.
 XX Human homolog of the Drosophila suppressor of fused gene useful in the
 PT treatment of Split hand/Split foot Malformation Type 3.
 XX Example; Page 67; 82pp; English.
 XX The invention relates to proteins, polypeptides and nucleotides related
 CC to the human homologue of the Drosophila suppressor of fused gene, which
 CC is involved in the transduction of signals in the human hedgehog-patched
 CC (HH-PTC) pathway. Protein molecule capable of eliciting an intracellular
 CC signal in the HH-PTC pathway, its antibodies and pharmaceutical
 CC compositions comprising them can be used as medicaments for the treatment
 CC and/or prevention of split hand/split foot malformation type 3 (SHFM3).
 CC The polynucleotides and polypeptides of the invention can be used to gain
 CC an understanding of a signalling pathway that is central to normal
 CC development and often disrupted in disease. This knowledge will be value
 CC for therapeutic strategies involving modification of sonic hedgehog-
 CC patched (SHH-PTC) signalling pathway. Potential areas include
 CC tissue/wound healing, neurodegenerative diseases, testicular function and
 CC cancer. The polynucleotides of the invention may also be used in gene
 CC therapy methods. The present sequence is a rapid amplification of cDNA
 CC ends (RACE) PCR primer used for cloning human SU(FU) homologue. This
 CC sequence is used in the exemplification of the invention
 XX
 SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 19.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 47;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 58 GAAGCTGATGCTCTGTCA 75
 DB 1 GAAGCTGATGCTACTGCCA 18
 RESULT 27
 ADT92489
 ID ADT92489 standard; DNA; 21 BP.
 XX ADT92489;
 XX 16-DEC-2004 (first entry)
 XX Human suppressor of fused (SU(FU)) primer seqid 3.
 XX cytostatic; neuroprotective; suppressor of fused; SUFU;
 KW signal transduction; patched receptor; hedgehog ligand;
 KW hedgehog-patched pathway; HH-PTC pathway;
 KW Split hand/Split foot Malformation Type 3; SHFM3; sonic hedgehog-patched;
 KW SHH-PTC signal pathway; tissue healing; wound healing;
 KW neurodegenerative disease; testicular function; cancer; gene therapy;
 KW human; SUFUH; PCR; primer; ss.
 XX Homo sapiens.
 XX US6448020-B1.
 XX 10-SEP-2002.
 XX 21-AUG-2000; 2000US-00581831.
 XX 19-DEC-1997; 97SE-00004788.
 PR 26-JUN-1998; 98SE-00002293.
 PR

PR 18-DEC-1998; 98WO-SR002383.
 XX (TOFT/) TOFTGARD R.
 PA (ZAPH/) ZAPHIROPOULOS P. G.
 PA (KOG/) KOGERMAN P.
 XX
 XX Toftgard R, Zaphiropoulos PG, Kogerman P, Grimm T;
 XX WPI; 1999-405160/34.
 XX
 XX Human homolog of the Drosophila suppressor of fused gene useful in the
 PT treatment of Split hand/Split foot Malformation Type 3.
 PT
 XX Example; SEQ ID NO 3; 37pp; English.
 PS
 XX The invention describes novel human homologues to molecules associated
 CC with the Drosophila suppressor of fused (SUFU) gene. These molecules are
 CC implicated in the transduction of the signals that are elicited by the
 CC interaction between the patched receptor and any one of the hedgehog
 CC ligands. Also described are: an isolated protein molecule (I) capable of
 CC eliciting an intracellular signal in the human hedgehog-patched (HH-PTC)
 CC pathway and exhibiting a substantial similarity (especially about 80%),
 CC the amino acid sequence is not given in the specification; an isolated
 CC human DNA sequence (II) capable of involvement in eliciting an
 CC intracellular signal in the HH-PTC pathway, the nucleotide sequence is
 CC not given in the specification; a DNA sequence encoding the protein of
 CC (I) or their variants; a vector comprising (II) or the DNA sequence (3);
 CC an expression cassette comprising (II) or the DNA sequence (3); a cell
 CC comprising the expression cassette of (5); an antibody that binds
 CC specifically to (I); a recombinant cell expressing the antibody of (7); a
 CC kit for the detection of a human suppressor of fused gene, comprising a
 CC nucleic acid sequence capable of hybridising specifically with (II); and
 CC a kit for the detection of a protein encoded by the human suppressor of
 CC fused gene, comprising a container containing the antibody of (7). (I),
 CC its antibodies and pharmaceutical compositions comprising them can be
 CC used as medicaments for the treatment and/or prevention of Split
 CC hand/Split foot Malformation Type 3 (SHFM3). The polynucleotides and
 CC polypeptides can be used to gain an understanding of a signaling pathway
 CC that is central to normal development and often disrupted in disease.
 CC This knowledge will be value for therapeutic strategies involving
 CC modification of sonic hedgehog-patched (SHH-PTC) signaling pathway.
 CC Potential areas include tissue/wound healing, neurodegenerative diseases,
 CC testicular function and cancer. The polynucleotide may also be used in
 CC gene therapy methods. This sequence represents a primer used to isolate
 CC DNA encoding human suppressor of fused (SUFUH).
 XX
 SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
 Query Match 19.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 47;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 58 GAAGCTGATCTCTGTCA 75
 Db 1 GAAGCTGATCTCTGTCCA 18
 |||||
 RESULT 28
 ADS93548/c
 ID ADS93548 standard; RNA; 21 BP.
 XX
 XX ADS93548;
 AC
 XX
 DT 02-DEC-2004 (first entry)
 XX
 XX Human MRCK2 siRNA sequence SeqID14.
 DE
 XX human protein kinase; MCRK2;
 KW myotonic dystrophy kinase-related Cdc42 binding kinase 2; 1q42;
 KW chromosome 1; pkinase_C domain; DAG-PE; CNH domain;
 KW cytoskeleton reorganisation; cytosstatic; antinflammatory;
 KW antiarteriosclerotic; ophthalmological; antipsoriatic; antiasthmatic;
 KW antiparkinsonian; antirheumatic; antiarthritic; neuroprotective;

KW muscular-Gen; osteopathic; cardiovascular-Gen; immunosuppressive;
 KW cerebroprotective; vasotropic; anticonvulsant; anti-HIV; MRCK2-modulator;
 KW gene therapy; inflammation; cancer; arteriosclerosis; psoriasis; asthma;
 KW Parkinson's disease; rheumatoid arthritis; spinal cord injury;
 KW muscle condition; osteoporosis; graft versus host disease;
 KW cardiovascular disorder; autoimmune disorder; retinal detachment; stroke;
 KW epilepsy; ischaemia; reperfusion; breast cancer; ovarian cancer;
 KW glioblastoma; non-Hodgkin's lymphoma; colorectal cancer;
 KW non-small cell lung cancer; brain cancer; Kaposi's sarcoma;
 KW pancreatic cancer; liver cancer; tumour; siRNA; short interfering RNA;
 KW human; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO2004033638-A2.
 PN
 XX 22-APR-2004.
 PD
 XX 07-OCT-2003; 2003WO-US031591.
 PF
 XX 07-OCT-2002; 2002US-0416257P.
 PR
 XX (AMHP) WYETH.
 PA (LIUW/) LIU W.
 PA (WULW/) WU L.
 XX
 XX Liu W, Wu L;
 PI
 XX WPI; 2004-340908/31.
 DR
 XX New isolated polypeptide, useful for preventing or treating a myotonic
 XX dystrophy kinase-related Cdc42 binding kinase 2 (MRCK2)-related disease
 PT e.g., inflammation, cancer, arteriosclerosis, psoriasis, and Parkinson's
 PT disease.
 PT
 XX Disclosure; SEQ ID NO 14; 242pp; English.
 PS
 XX This invention relates to a novel isolated human protein kinase, MCRK2.
 CC The sequence shows homology to rat myotonic dystrophy kinase-related
 CC Cdc42 binding kinase 2 (MRCK2). The gene encoding the novel kinase is
 CC localised to human 1q42 of human chromosome 1. The novel protein
 CC kinase comprises multiple functional/structural domains that include a
 CC kinase domain, a pkinase_C domain, a DAG-PE binding domain and a CNH
 CC domain. The protein may function as a downstream effector of Cdc42 in
 CC cytoskeleton reorganisation. The invention may be useful for the
 CC production of cytostatic, antiinflammatory, antiarteriosclerotic,
 CC ophthalmological, antipsoriatic, antiasthmatic, antiparkinsonian,
 CC antirheumatic, antiarthritic, neuroprotective, muscular-Gen, osteopathic,
 CC cardiovascular-Gen, immunosuppressive, cerebroprotective, vasotropic,
 CC anticonvulsant or anti-HIV activity acting as myotonic dystrophy kinase-
 CC related Cdc42 binding kinase 2 (MRCK2)-inhibitors or MRCK2-Modulator. In
 CC addition, the disclosed sequences may be used for gene therapy. The
 CC invention may be useful for preventing or treating an myotonic dystrophy
 CC kinase-related Cdc42 binding kinase 2 (MRCK2)-related disease in a
 CC subject such as inflammation, cancer, arteriosclerosis, psoriasis,
 CC asthma, Parkinson's disease, rheumatoid arthritis, spinal cord injuries,
 CC muscle conditions, osteoporosis, graft versus host disease,
 CC cardiovascular disorders, autoimmune disorders, retinal detachment,
 CC stroke, epilepsy, ischaemia/reperfusion, breast cancer, ovarian cancer,
 CC glioblastoma, non-Hodgkin's lymphoma, colorectal cancer, non-small cell
 CC lung cancer, brain cancer, Kaposi's sarcoma, pancreatic cancer, liver
 CC cancer and other tumours. The MRCK2 and MRCK2 gene are useful as models
 CC for the development of human therapeutic targets, aid in the
 CC identification of therapeutic proteins, and serve as targets for the
 CC development of human therapeutic agents that modulate kinase activity in
 CC cells and tissues that express the kinase. The present sequence is that
 CC of a short interfering RNA (siRNA) molecule which was designed to target
 CC the human MRCK2 coding sequence and which is related to the invention.
 XX
 SQ Sequence 21 BP; 5 A; 4 C; 5 G; 0 T; 7 U; 0 Other;
 Query Match 19.2%; Score 14.8; DB 1; Length 21;
 Best Local Similarity 88.9%; Pred. No. 47;

Query Match 18.7%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 42;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42
 DB 2 TCTGGAGTCTCTGTG 17

RESULT 31
 ABN10035
 ID ABN10035 standard; DNA; 17 BP.
 XX AC ABN10035;
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10027.
 XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX OS Homo sapiens.
 XX PN WO200192524-A2.
 XX PD 06-DEC-2001.
 XX PF 25-MAY-2001; 2001WO-US016981.
 XX PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX DR
 XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX PS
 XX PS Disclosure; SEQ ID NO 10027; 214pp; English.
 XX CC
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP-
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The

CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 18.7%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 42;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTGAG 42
 DB 1 TCTGGAGTCTCTGTG 16

RESULT 32
 ACN73125
 ID ACN73125 standard; DNA; 17 BP.
 XX AC ACN73125;
 XX DT 02-DEC-2004 (first entry)
 XX DE Human GDMPLP-1 probe SEQ ID NO:10027.
 XX KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX OS Homo sapiens.
 XX PN US2004137589-A1.
 XX PD 15-JUL-2004.
 XX PF 26-NOV-2003; 2003US-00723361.
 XX PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX PS
 XX PS (GUY/) GU Y.
 XX PA (JIY/) JI Y.
 XX PA (PENN/) PENN S G.
 XX PA (HANZ/) HANZEL D K.
 XX PA (RANK/) RANK D.
 XX PA (CHEN/) CHEN W.
 XX PA (SHAN/) SHANNON M E.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 XX DR
 XX PT Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived

PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 XX function.
 PS Disclosure; SEQ ID NO 10027; Opp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 18.7%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 42;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 27 TCTGGAGTCTCTCTGAG 42
 Db 1 TCTGGAGTCTCTCTGTG 16
 RESULT 33
 ACN73124
 ID ACN73124 standard; DNA; 17 BP.
 XX
 AC ACN73124;
 DT 02-DEC-2004 (first entry)
 XX
 DE Human GDMLP-1 probe SEQ ID NO:10026.
 XX
 KW Human; ss; probe; myosin-like protein-1; hGDMLP-1;
 KW hGDMLP-1 agonist hGDMLP antagonist; hGDMLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 OS Homo sapiens.
 XX
 PN US2004137589-A1.
 XX
 PD 15-JUL-2004.
 XX
 PF 26-NOV-2003; 2003US-00723361.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001WO-US000670P.
 PR 25-MAY-2001; 2001US-00866108.
 XX
 PA (GUY/) GU Y.
 PA (JIY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANZ/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.

PA (SHAN/) SHANNON M E.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 DR
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 PS Disclosure; SEQ ID NO 10026; Opp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMLP-1, or as an inhibitor of hGDMLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 18.7%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 42;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 27 TCTGGAGTCTCTCTGAG 42
 Db 2 TCTGGAGTCTCTCTGTG 17
 RESULT 34
 AAZ31818/c
 ID AAZ31818 standard; DNA; 18 BP.
 XX
 AC AAZ31818;
 XX
 DT 24-JAN-2000 (first entry)
 XX
 DE Human G-alpha-13 antisense inhibitor ISIS# 20767.
 XX
 KW G-alpha-13; human; inhibitor; cancer; antisense compound; therapy; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5981732-A.
 XX
 PD 09-NOV-1999.
 XX
 PF 04-DEC-1998; 98US-00205860.
 XX
 PR 04-DEC-1998; 98US-00205860.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Cowbert LM;
 XX
 DR WPI; 1999-633376/54.
 XX
 PT Antisense compound inhibiting expression of human G-alpha-13.
 XX
 PS Claim 11; Col 39; 38pp; English.
 XX
 CC This sequence represents an antisense inhibitor of the invention, and
 CC inhibits the expression of the human G-alpha-13 protein. The antisense
 CC compounds of the invention are of 8 to 30 nucleobases in length, that
 CC inhibits the expression of the human G-alpha-13. The antisense compound

CC is useful for treating an animal, particularly humans, having or being
 CC prone to a disease or condition associated with the expression of G-alpha
 CC -13, such as cancer

XX
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 18.7%; Score 14.4; DB 1; Length 18;
 Best Local Similarity 93.8%; Pred. No. 45;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 CCTGGGGATACAACTC 28
 Db 17 CCTGGGGAGACAACTC 2

RESULT 35
 ADK74660/C
 ID ADK74660 standard; DNA; 20 BP.

XX
 AC ADK74660;
 XX
 DT 20-MAY-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #1994.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
 KW diabetic neuropathy; arthritic pain; migraine headache;
 KW infantile epilepsy; ataxia; ss.

XX Synthetic.

XX WO2004016754-A2.

XX
 PD 26-FEB-2004.

XX 14-AUG-2003; 2003WO-US025465.

XX 14-AUG-2002; 2002US-0403416P.

XX (PHAA) PHARMACIA CORP.

XX Roberds SL;

XX WPI; 2004-203785/19.

XX New antisense compound targeted to a nucleic acid molecule encoding
 PT Nav1.3, useful for treating a disease or condition associated
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
 PT disorder, or ataxia.

XX Claim 4; SEQ ID NO 1994; 417pp; English.

XX The present invention relates to an antisense compound targeted to a
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The
 CC compound and composition are useful for treating a disease or condition
 CC associated with Nav1.3, e.g. pain including but not limited to
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate
 CC headache; seizure disorder such as childhood seizure disorder, including
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
 CC sequence represents a chimeric phosphorothioate oligonucleotide with
 CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of
 CC human Nav1.3 expression, the oligonucleotides are designed to target
 CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 18.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 55;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 36 CTCCTGAGAGCTAAAGACC 54
 Db 20 CTCCTGAGAGCTAAAGACC 2

RESULT 36

ADK73231/C

ID ADK73231 standard; DNA; 20 BP.

XX
 AC ADK73231;

XX 20-MAY-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide to target Nav1.3 #565.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
 KW diabetic neuropathy; arthritic pain; migraine headache;
 KW infantile epilepsy; ataxia; ss.

XX Synthetic.

XX WO2004016754-A2.

XX
 PD 26-FEB-2004.

XX 14-AUG-2003; 2003WO-US025465.

XX 14-AUG-2002; 2002US-0403416P.

XX (PHAA) PHARMACIA CORP.

XX Roberds SL;

XX WPI; 2004-203785/19.

XX New antisense compound targeted to a nucleic acid molecule encoding
 PT Nav1.3, useful for treating a disease or condition associated
 PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
 PT disorder, or ataxia.

XX Claim 4; SEQ ID NO 565; 417pp; English.

XX The present invention relates to an antisense compound targeted to a
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The
 CC compound and composition are useful for treating a disease or condition
 CC associated with Nav1.3, e.g. pain including but not limited to
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate
 CC headache; seizure disorder such as childhood seizure disorder, including
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
 CC sequence represents a chimeric phosphorothioate oligonucleotide with
 CC 2' MOE wings and a deoxy gap. Used during the antisense inhibition of
 CC human Nav1.3 expression, the oligonucleotides are designed to target
 CC different regions of the human Nav1.3 RNA.

XX Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 18.4%; Score 14.2; DB 1; Length 20;
 Best Local Similarity 84.2%; Pred. No. 55;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGCTAAAGAG 52
 Db 19 TCCTCTGAGAGCTAAAGAG 1

RESULT 37

ADP12043/C

ID ADP12043 standard; DNA; 20 BP.

XX
 AC ADP12043;

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XX 12-AUG-2004 (first entry)
XX Set 2 right PCR primer for marker probe #149.
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.
XX Homo sapiens.
XX WO2004042346-A2.
XX 21-MAY-2004.
XX 24-APR-2003; 2003WO-US012946.
XX 24-APR-2002; 2002US-00131831.
XX 20-DEC-2002; 2002US-00325999.
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M,
XX Rosenberg S;
XX WPI; 2004-400724/37.
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX rejection, in an individual, comprises detecting the expression level of
XX the genes.
XX Claim 58; SEQ ID NO 2052; 1762pp; English.
XX The present invention relates to diagnosing or monitoring transplant
XX rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX comprises detecting the expression level of one or more genes. The
XX methods, system and kits are useful in diagnosing or monitoring
XX transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX islet, lung, bone marrow or stem cell transplant rejection,
XX xenotransplant rejection or mechanical organ replacement rejection, in an
XX individual. The method is also useful in assessing the immune status of
XX an individual. The methods are also useful in diagnosing and monitoring
XX diseases that involve the immune system, e.g. rheumatoid arthritis,
XX lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX viral, bacterial or fungal infection. The present sequence represents a
XX primer for a 50 mer oligonucleotide marker for diagnosis and monitoring
XX of allograft rejection and other disorders.
XX Sequence 20 BP; 2 A; 5 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 18.4%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 32 AGTCCTCTGAGAGGTAAG 50
DB 20 ACTCTCCGAGGCGCAAG 2
RESULT 38
ABN10033
ID ABN10033 standard; DNA; 17 BP.
XX AC ABN10033;
XX 29-MAY-2002 (first entry)
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10025.
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.

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OS Homo sapiens.
XX WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 05-FEB-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX (ABOM-) ABOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 10025; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX Sequence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
Query Match 18.2%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 TCTGGAGTCTCTG 40
DB 3 TCTGGAGTCTCTG 16
RESULT 39
ABN10032
ID ABN10032 standard; DNA; 17 BP.

```

XX AC ABN10032;
 XX DT 29-MAY-2002 (first entry)
 XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10024.
 XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX OS Homo sapiens.
 XX PN WO200192524-A2.
 XX PD 06-DEC-2001.
 XX PF 25-MAY-2001; 2001WO-US016981.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 30-JAN-2001; 2001WO-US000670.
 XX PR 05-FEB-2001; 2001US-0266860P.
 XX PA (AEOM-) AEOMICA INC.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX DT WPI; 2002-179446/23.
 XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX PS Disclosure; SEQ ID NO 10024; 214pp; English.
 XX CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pt_sequence
 XX SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 18.2%; Score 14; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 49;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TCTGGAGTCTCTG 40
 DB 4 TCTGGAGTCTCTG 17
 RESULT 40
 ACN73122
 ID ACN73122 standard; DNA; 17 BP.
 XX AC ACN73122;
 XX DT 02-DEC-2004 (first entry)
 XX DE Human GDMPLP-1 probe SEQ ID NO:10024.
 XX KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX OS Homo sapiens.
 XX PN US2004137589-A1.
 XX PD 15-JUL-2004.
 XX PF 26-NOV-2003; 2003US-00723361.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 05-FEB-2001; 2001US-0266860P.
 XX PR 25-MAY-2001; 2001US-00866108.
 XX PA (GUYI/) GU Y.
 XX PA (JIYY/) JI Y.
 XX PA (PENNY/) PENN S G.
 XX PA (HANZ/) HANZEL D K.
 XX PA (RANK/) RANK D.
 XX PA (CHEN/) CHEN W.
 XX PA (SHAN/) SHANNON M E.
 XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX DT WPI; 2004-533378/51.
 XX PT Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX PS Disclosure; SEQ ID NO 10024; 0pp; English.
 XX CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or

CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 Query Match 18.2%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TCTGGAGTCTCTCG 40
 |||||
 Db 4 TCTGGAGTCTCTCG 17
 RESULT 41
 ACN73123
 ID ACN73123 standard; DNA; 17 BP.
 XX
 AC ACN73123;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Human GDMPLP-1 probe SEQ ID NO:10025.
 XX
 KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX
 OS Homo sapiens.
 XX
 PN US2004137589-A1.
 XX
 PD 15-JUL-2004.
 XX
 PF 26-NOV-2003; 2003US-00723361.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US0008661.
 PR 30-JAN-2001; 2001WO-US0008662.
 PR 30-JAN-2001; 2001WO-US0008663.
 PR 30-JAN-2001; 2001WO-US0008664.
 PR 30-JAN-2001; 2001WO-US0008665.
 PR 30-JAN-2001; 2001WO-US0008666.
 PR 30-JAN-2001; 2001WO-US0008667.
 PR 30-JAN-2001; 2001WO-US0008668.
 PR 30-JAN-2001; 2001WO-US0008669.
 PR 05-FEB-2001; 2001US-0266860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX
 PA (GUYY/) GU Y.
 PA (JIYV/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANK/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 XX
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 PS Disclosure; SEQ ID NO 10025; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence
 CC (SI) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (SI), 95% deviation from (SI) which are conservative substitutions, and
 CC 65% identity to (SI). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 1 A; 4 C; 5 G; 7 T; 0 U; 0 Other;
 Query Match 18.2%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 27 TCTGGAGTCTCTCG 40
 |||||
 Db 3 TCTGGAGTCTCTCG 16
 RESULT 42
 ADC04443/c
 ID ADC04443 standard; DNA; 17 BP.
 XX
 AC ADC04443;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human Na/H exchanger-like protein 1 gene oligonucleotide #890.
 XX
 KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
 KW NHEPLP1; passive replacement therapy; vaccine; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN EP1273660-A2.
 XX
 PD 08-JAN-2003.
 XX
 PF 25-JAN-2002; 2002EP-00001160.
 XX
 PR 30-JAN-2001; 2001WO-US000666.
 PR 23-MAY-2001; 2001US-00864761.
 PR 21-DEC-2001; 2001US-0343331P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y;
 XX
 DR WPI; 2003-302724/30.
 XX
 PT New human sodium-hydrogen exchanger like protein 1 (NHEPLP1), useful as a
 PT passive replacement therapy or as a vaccine for treating or preventing
 PT disorders associated with aberrant expression or activity of human
 PT NHEPLP1.
 XX
 PS Example 2; SEQ ID NO 930; 468pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which encodes a Na/H+
 CC exchanger like protein (NHEPLP1). The NHEPLP1 nucleic acid molecule, NHEPLP1
 CC polypeptide, an antibody against the protein or its antigen-binding
 CC fragment is useful in therapy. The NHEPLP1 nucleic acid molecule, NHEPLP1
 CC polypeptide and an agonist are particularly useful for manufacturing a
 CC medicament for treating or preventing a disorder associated with
 CC decreased expression or activity of human NHEPLP1. The antibody or its
 CC antigen-binding fragment, and an antagonist, are useful for manufacturing
 CC a medicament for treating or preventing a disorder associated with
 CC increased expression or activity of human NHEPLP1. The NHEPLP1 nucleic acid
 CC or protein is useful as passive replacement therapy, as a vaccine, or in

CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
CC spanning the sequence of the human NHEP1 gene (ADC03514).

XX Sequence 17 BP; 2 A; 5 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 17.9%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 47 AAAGAGCCAGCGAAGCT 63
DB 17 AATGAGCCAGCGAAGAT 1

RESULT 43
ADJ82395
ID ADJ82395 standard; DNA; 15 BP.
XX AC ADJ82395;
XX DT 06-MAY-2004 (first entry)
XX DE KLMXY-encoding nucleotide #123.

XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
KW myeloproliferative disease; blood vessel proliferative disease;
KW angiogenesis.

XX Synthetic.
XX PN WO2003045973-A2.
XX PD 05-JUN-2003.
XX PF 30-SEP-2002; 2002WO-US031165.
XX PR 28-NOV-2001; 2001US-0333476P.
XX PA (BECT) BECTON DICKINSON & CO.
XX PA (HAAL/) HAALAND P D.
XX PI Dean C, Heidaran M, Spargo CA;
XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor
PT or cancer cell proliferation, or for treating fibrotic disorders,
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
PT disorders.

PS Disclosure; SEQ ID NO 176; 48pp; English.
XX The invention relates to an isolated peptide or polypeptide (I) of no
CC more than about 50 amino acid residues which when contacted with cells in
CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
CC an autocrine manner, inhibits the growth of these cells. The isolated
CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell
CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
CC muscle or bone cell. The peptides are also useful for treating fibrotic
CC disorders, myeloproliferative diseases, and blood vessel proliferative
CC (angiogenic) disorders. This sequence represents a possible nucleotide
CC encoding the P3 peptide.

XX Sequence 15 BP; 4 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 17.4%; Score 13.4; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 52;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGCTCTGT 73
DB 1 AAGCTGATGCTCTAT 15

RESULT 44
ABN10036
ID ABN10036 standard; DNA; 17 BP.
XX AC ABN10036;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10028.

XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

XX Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US015981.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 05-FEB-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX PA (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
PS Disclosure; SEQ ID NO 10028; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a

CC disorder associated with the expression of hGDMPL-1, in particular heart
 CC and skeletal muscle disorders. hGDMPL-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPL-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 17.4%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 61;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCCTCTGAG 42
 Db 1 CTGGAGTCCTCTGTG 15

RESULT 45
 ID ABT38020 standard; DNA; 17 BP.
 XX AC
 AC ABT38020;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 3657.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 PN W02003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004208.
 XX
 PR 17-SEP-2001; 2001FR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 461; 720pp; French.
 XX

CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti-) sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these

CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention
 XX
 SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 17.4%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 61;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCCTCTGAGA 43
 Db 17 TGGAGTCCTCTGAGA 3

RESULT 46
 ADC04444/C
 ID ADC04444 standard; DNA; 17 BP.
 XX AC
 AC ADC04444;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human Na/H exchanger-like protein 1 gene oligonucleotide #891.
 XX
 KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
 KW NHEPLP1; passive replacement therapy; vaccine; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN EP1273660-A2.
 XX
 PD 08-JAN-2003.
 XX
 PF 25-JAN-2002; 2002EP-00001160.
 XX
 PR 30-JAN-2001; 2001WO-US000666.
 PR 23-MAY-2001; 2001US-00864761.
 PR 21-DEC-2001; 2001US-0343331P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y;
 XX
 DR WPI; 2003-302724/30.
 XX
 PT New human sodium-hydrogen exchanger like protein 1 (NHEPLP1), useful as a
 PT passive replacement therapy or as a vaccine for treating or preventing
 PT disorders associated with aberrant expression or activity of human
 PT NHEPLP1.
 XX
 PS Example 2; SEQ ID NO 931; 468pp; English.
 XX

CC The invention relates to a nucleic acid molecule which encodes a Na+/H+
 CC exchanger like protein (NHEPLP1). The NHEPLP1 nucleic acid molecule, NHEPLP1
 CC polypeptide, an antibody against the protein or its antigen-binding
 CC fragment is useful in therapy. The NHEPLP1 nucleic acid molecule, NHEPLP1
 CC polypeptide and an agonist are particularly useful for manufacturing a
 CC medicament for treating or preventing a disorder associated with
 CC decreased expression or activity of human NHEPLP1. The antibody or its
 CC antigen-binding fragment, and an antagonist, are useful for manufacturing
 CC a medicament for treating or preventing a disorder associated with
 CC increased expression or activity of human NHEPLP1. The NHEPLP1 nucleic acid
 CC or protein is useful as passive replacement therapy, as a vaccine, or in
 CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
 CC spanning the sequence of the human NHEPLP1 gene (ADC03514).
 XX
 SQ Sequence 17 BP; 1 A; 5 C; 3 G; 8 T; 0 U; 0 Other;
 Query Match 17.4%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 61;

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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 47 AAAGAGCCAGCGAAG 61
Db 16 AATGAGCCAGCGAAG 2

RESULT 47
ADC04445/c
ID ADC04445 standard; DNA; 17 BP.
XX AC ADC04445;
XX AC
XX DT 18-DEC-2003 (first entry)
XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #892.
XX KW ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
XX KW NHEP1; passive replacement therapy; vaccine; diagnosis.
XX OS Homo sapiens.
XX PN BP1273660-A2.
XX PD 08-JAN-2003.
XX PP 25-JAN-2002; 2002EP-00001160.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 21-DEC-2001; 2001US-0343331P.
XX PA (AEOM-) AEOMICA INC.
XX PI
XX PT Gu Y;
XX DR WPI; 2003-302724/30.
XX PT New human sodium-hydrogen exchanger like protein 1 (NHEP1), useful as a
XX PT passive replacement therapy or as a vaccine for treating or preventing
XX PT disorders associated with aberrant expression or activity of human
XX PT NHEP1.
XX PS Example 2; SEQ ID NO 932; 468pp; English.
XX CC The invention relates to a nucleic acid molecule which encodes a Na+/H+
XX CC exchanger like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1
XX CC polypeptide, an antibody against the protein or its antigen-binding
XX CC fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1
XX CC polypeptide and an agonist are particularly useful for manufacturing a
XX CC medicament for treating or preventing a disorder associated with
XX CC decreased expression or activity of human NHEP1. The antibody or its
XX CC antigen-binding fragment, and an antagonist, are useful for manufacturing
XX CC a medicament for treating or preventing a disorder associated with
XX CC increased expression or activity of human NHEP1. The NHEP1 nucleic acid
XX CC or protein is useful as passive replacement therapy, as a vaccine, or in
XX CC diagnostic methods. This sequence corresponds to a 17-near oligonucleotide
XX CC spanning the sequence of the human NHEP1 gene (ADC03514).
XX SQ Sequence 17 BP; 1 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 61;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 47 AAAGAGCCAGCGAAG 61
Db 15 AATGAGCCAGCGAAG 1

RESULT 48
ADB45419/c
ID ADB45419 standard; DNA; 17 BP.

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```

XX ADB45419;
XX AC
XX DT 18-DEC-2003 (first entry)
XX DE Tumour suppression/reversion associated nucleotide #5742.
XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX KW primer; probe; tumour suppression; tumour reversion; apoptosis;
XX KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX KW diagnosis.
XX OS Homo sapiens.
XX PN WO2003040369-A2.
XX PD 15-MAY-2003.
XX PF 17-SEP-2002; 2002WO-IB004219.
XX PR 17-SEP-2001; 2001FR-00011981.
XX PA (MOLR-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-441574/41.
XX PT New nucleic acid encoding human prostate membrane-specific antigen,
XX PT useful e.g. for treatment of tumors and viral infection, also related
XX PT polypeptide and antibodies.
XX PS Disclosure; Page 703; 771pp; French.
XX CC The invention relates to the isolation of 6377 nucleotide sequences,
XX CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX CC sequence having at least 80% identity, after optimal alignment, with the
XX CC nucleotides, a sequence that hybridizes under stringent conditions with
XX CC the nucleotides, or the complement, or corresponding RNA, of the
XX CC nucleotides. The nucleotides are used as probes or primers for detecting,
XX CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
XX CC sense and antisense sequences, of nucleotides involved in tumour
XX CC suppression or reversion, apoptosis and or viral resistance, to produce
XX CC recombinant polypeptides, and to prepare transgenic animals, as
XX CC experimental models. The nucleotides (also vectors containing them and
XX CC cells containing the vectors), the encoded polypeptides and antibodies
XX CC (Ab) against the polypeptide are useful for prevention and/or treatment
XX CC of viral infections or diseases characterized by development of tumours
XX CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
XX CC Analysis of the expression of the nucleotides can be used for diagnosis
XX CC and/or prognosis of these diseases. The nucleotides and polypeptides can
XX CC also be used to screen for their specific interactive molecules,
XX CC potentially useful for treating diseases associated with abnormal
XX CC expression of the nucleotides.
XX SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 17.4%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 61;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 29 TGGAGTCTCTGAGA 43
Db 17 TGGAGTCTCTGAGA 3

RESULT 49
ADI51144/c
ID ADI51144 standard; DNA; 17 BP.
XX AC ADI51144;
XX DT 15-APR-2004 (first entry)

```


XX DE Human tumour suppression/reversion-related DNA sequence SeqID3647.
 XX XX
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytosstatic; virucide; neuroprotective; nontropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX OS Homo sapiens.
 XX XX WO2003025177-A2.
 XX XX 27-MAR-2003.
 XX PF 17-SEP-2002; 2002WO-IB004523.
 XX XX 17-SEP-2001; 2001FR-00011980.
 XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX XX Telerman A, Amson R, Tuijnder M;
 XX XX WPI; 2003-313354/30.
 XX DR New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX XX Disclosure; SEQ ID NO 3647; 30pp; French.
 XX CC This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC nontropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration.
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX XX
 XX SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 17.4%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 61;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 29 TGGAGTCTCTGAGA 43
 DB 17 TGGAGTCTCTGAGA 3
 RESULT 50
 ACN73126
 ID ACN73126 standard; DNA; 17 BP.
 XX AC ACN73126;
 XX DT 02-DEC-2004 (first entry)
 XX DE Human GDMPL-1 probe SEQ ID NO:10028.
 XX KW Human; ss; probe; myosin-like protein-1; hGDMPL-1;
 KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;
 KW skeletal muscle function.
 XX OS Homo sapiens.
 XX XX US2004137589-A1.
 XX XX 15-JUL-2004.
 XX PF 26-NOV-2003; 2003US-00723361.
 XX XX 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX OS Homo sapiens.

XX PN FR2826373-A1.
 XX PD 27-DEC-2002.
 XX PF 20-JUN-2001; 2001FR-00008139.
 XX PR 20-JUN-2001; 2001FR-00008139.
 XX PA (MOLE-) MOLECULAR ENGINES LAB SA.
 XX XX Tuijnder M, Telerman A, Amson R;
 XX XX WPI; 2003-250498/25.
 XX DR New nucleic acid sequences associated with tumour suppression, regression,
 PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.
 XX PS Claim 1; Page 612; 798pp; French.
 XX CC This sequence represents an isolated nucleic acid sequence associated
 CC with tumour suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 XX XX
 XX SQ Sequence 17 BP; 6 A; 5 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 17.4%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 61;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 29 TGGAGTCTCTGAGA 43
 DB 17 TGGAGTCTCTGAGA 3
 RESULT 51
 ACN73126
 ID ACN73126 standard; DNA; 17 BP.
 XX AC ACN73126;
 XX DT 02-DEC-2004 (first entry)
 XX DE Human GDMPL-1 probe SEQ ID NO:10028.
 XX KW Human; ss; probe; myosin-like protein-1; hGDMPL-1;
 KW hGDMPL-1 agonist hGDMPL antagonist; hGDMPL inhibitor; heart disorder;
 KW skeletal muscle function.
 XX OS Homo sapiens.
 XX XX US2004137589-A1.
 XX XX 15-JUL-2004.
 XX PF 26-NOV-2003; 2003US-00723361.
 XX XX 26-MAY-2000; 2000US-0207456P.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0236359P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PR 30-JAN-2001; 2001WO-US000661.
 XX PR 30-JAN-2001; 2001WO-US000662.
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX OS Homo sapiens.

PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 03-FEB-2001; 2001US-0266860P.
 PR 25-MAY-2001; 2001US-00866108.
 XX
 PA (GUYV/) GU Y.
 PA (JIVV/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANKZ/) HANZEL D K.
 PA (RANKZ/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 XX WPI; 2004-533378/51.
 DR
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX
 PS Disclosure; SEQ ID NO 10028; 0pp; English.
 XX
 CC The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGMDLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGMDLP-1, or as an inhibitor of hGMDLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGMDLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 17.4%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 61;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 28 CTGAGTCCCTCGAG 42
 Db |||||
 1 CTGAGTCCCTCGTG 15
 RESULT 52
 AAQ55741/C
 ID AAQ55741 standard; DNA; 18 BP.
 XX
 AC AAQ55741;
 XX
 XX 25-MAR-2003 (revised)
 DT 22-JUL-1994 (first entry)
 XX
 DE LCR Oligo A.
 XX
 KW Ligase chain reaction; LCR; Pyrococcus furiosus; ligation; Pfu;
 KW hyperthermophilic archaeobacterium; catalysis; blunt-end; Tth;
 KW Thermus thermophilus; ss.
 XX
 OS Synthetic.
 XX
 XX WO9402615-A1.
 XX
 PD 03-FEB-1994.
 XX
 XX 22-JUL-1993; 93WO-US0006939.
 DT 22-JUL-1994 (first entry)
 XX
 DE LCR Oligo A.
 XX
 KW Ligase chain reaction; LCR; Pyrococcus furiosus; ligation; Pfu;
 KW hyperthermophilic archaeobacterium; catalysis; blunt-end; Tth;
 KW Thermus thermophilus; ss.
 XX
 OS Synthetic.
 XX
 XX WO9402615-A1.
 XX
 PD 03-FEB-1994.
 XX
 XX 22-JUL-1993; 93WO-US0006939.
 PF 23-JUL-1992; 92US-00919140.
 XX
 PR 23-JUL-1992; 92US-00919140.
 XX

PA (STRA-) STRATAGENE.
 XX
 PI Mathur EJ, Marsh EJ, Schoettlin WE;
 XX WPI; 1994-048873/06.
 DR
 XX Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation
 PT specificity and stability at high temperatures, giving greater efficiency
 PT in ligase chain reaction.
 XX
 PS Example 12; Page 56; 84pp; English.
 XX
 CC Four oligonucleotide probes (AAQ55741-44) and two oligonucleotide
 CC templates (AAQ55739-40) were used in a ligase chain reaction of
 CC recombinant Pfu DNA ligase. The assay shows that both Tth DNA ligase and
 CC Pfu DNA ligase perform well in LCR after multiple cycles forming a single
 CC LCR DNA fragment without appreciable blunt-end ligation or background
 CC reaction prods. However, the Tth DNA ligase in not heat stable when
 CC exposed to temps. required to separate the strands of double-stranded
 CC genomic DNA. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 17.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 18 GGATACACTCTGGAGTC 35
 Db |||||
 18 GGACACACCTTGGAGTC 1
 RESULT 53
 AAQ55744
 ID AAQ55744 standard; DNA; 18 BP.
 XX
 AC AAQ55744;
 XX
 XX 25-MAR-2003 (revised)
 DT 22-JUL-1994 (first entry)
 XX
 DE LCR Oligo D.
 XX
 KW Ligase chain reaction; LCR; Pyrococcus furiosus; ligation; Pfu;
 KW hyperthermophilic archaeobacterium; catalysis; blunt-end; Tth;
 KW Thermus thermophilus; ss.
 XX
 OS Synthetic.
 XX
 XX WO9402615-A1.
 XX
 PD 03-FEB-1994.
 XX
 XX 22-JUL-1993; 93WO-US0006939.
 PF 23-JUL-1992; 92US-00919140.
 XX
 DE LCR Oligo D.
 XX
 PA (STRA-) STRATAGENE.
 XX
 PI Mathur EJ, Marsh EJ, Schoettlin WE;
 XX WPI; 1994-048873/06.
 DR
 XX Thermostable DNA ligase from Pyrococcus furiosus - has improved ligation
 PT specificity and stability at high temperatures, giving greater efficiency
 PT in ligase chain reaction.
 XX
 PS Example 12; Page 56; 84pp; English.
 XX
 CC Four oligonucleotide probes (AAQ55741-44) and two oligonucleotide
 CC templates (AAQ55739-40) were used in a ligase chain reaction of
 CC recombinant Pfu DNA ligase. The assay shows that both Tth DNA ligase and
 CC Pfu DNA ligase perform well in LCR after multiple cycles forming a single

```

CC LCR DNA fragment without appreciable blunt-end ligation or background
CC reaction prods. However, the Tth DNA ligase is not heat stable when
CC exposed to temps. required to separate the strands of double-stranded
CC genomic DNA. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACACCTTGGAGTC 18

RESULT 54
AAT14934/c
ID AAT14934 standard; DNA; 18 BP.
XX
AC AAT14934;
XX
XX 25-MAR-2003 (revised)
DT 26-SEP-1996 (first entry)
XX
XX Oligo A probe for Pfu DNA ligase LCR assay.
DE thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction;
KW LCR; template dependent ligation; ss.
XX
XX Synthetic.
XX
XX US5506137-A.
PN
XX 09-APR-1996.
PD
XX 22-JUL-1993; 93US-00096947.
PF
XX 23-JUL-1992; 92US-00919140.
PR
XX (STRA-) STRATAGENE.
PA
XX Schoettlin WE, Mathur EJ, Marsh EJ;
PI
XX WPI; 1996-200280/20.
XX
XX Plasmid contg. gene for thermostable DNA ligase - useful in ligase chain
XX reactions, stable up to 100 deg. C.
PT
XX Example 12; Col 25-26; 29pp; English.
PS
XX Recombinant Pyrococcus furiosus (Pfu) DNA ligase (AAR96967) activity was
CC assayed in a ligase chain reaction (LCR). The DNA templates consist of
CC two complementary 36-mer synthetic oligonucleotides (AAT14933). The
CC probes consist of 18-mer synthetic oligonucleotides (see AAT14934-37). The results
CC illustrated that both Tth and Pfu DNA ligase perform well in LCR after
CC multiple cycles forming a single LCR DNA fragment without appreciable
CC blunt-end ligation or background reaction products. Pfu DNA ligase was
CC able to perform well in LCR without a "pre-melting" step, whereas Tth DNA
CC ligase produced no detectable LCR product indicating that the Tth DNA
CC ligase is not heat stable when exposed to temperatures required to
CC separate the strands of double-stranded genomic DNA. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
XX Sequence 18 BP; 3 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 18 GGACACACCTTGGAGTC 1

RESULT 55
AAT14937
ID AAT14937 standard; DNA; 18 BP.
XX
XX AAT14937;
XX
XX 25-MAR-2003 (revised)
DT 26-SEP-1996 (first entry)
XX
XX Oligo D probe for Pfu DNA ligase LCR assay.
DE thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction;
KW LCR; template dependent ligation; ss.
XX
XX Synthetic.
XX
XX US5506137-A.
PN
XX 09-APR-1996.
PD
XX 22-JUL-1993; 93US-00096947.
PF
XX 23-JUL-1992; 92US-00919140.
PR
XX (STRA-) STRATAGENE.
PA
XX Schoettlin WE, Mathur EJ, Marsh EJ;
PI
XX WPI; 1996-200280/20.
XX
XX Plasmid contg. gene for thermostable DNA ligase - useful in ligase chain
XX reactions, stable up to 100 deg. C.
PT
XX Example 12; Col 25-26; 29pp; English.
PS
XX Recombinant Pyrococcus furiosus (Pfu) DNA ligase (AAR96967) activity was
CC assayed in a ligase chain reaction (LCR). The DNA templates consist of
CC two complementary 36-mer synthetic oligonucleotides (AAT14933). The
CC probes consist of 18-mer synthetic oligonucleotides (see AAT14934-37). The results
CC illustrated that both Tth and Pfu DNA ligase perform well in LCR after
CC multiple cycles forming a single LCR DNA fragment without appreciable
CC blunt-end ligation or background reaction products. Pfu DNA ligase was
CC able to perform well in LCR without a "pre-melting" step, whereas Tth DNA
CC ligase produced no detectable LCR product indicating that the Tth DNA
CC ligase is not heat stable when exposed to temperatures required to
CC separate the strands of double-stranded genomic DNA. (Updated on 25-MAR-
CC 2003 to correct PF field.)
XX
XX Sequence 18 BP; 5 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 17.1%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 69;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 GGATACAACTCTGGAGTC 35
Db 1 GGACACACCTTGGAGTC 18

RESULT 56
AAT13161/c
ID AAT13161 standard; DNA; 18 BP.
XX
XX AAT13161;
XX
XX 16-OCT-2001 (first entry)
DT
XX
XX Human MTSPI protease domain 5' end cDNA RACE sense PCR primer.
DE
XX Human; transmembrane serine protease; membrane-type serine protease;
KW MTSPI; protease domain; neoplastic disease; tumour; cancer; cytostatic;
KW

```

KW lung carcinoma; colon adenocarcinoma; ovarian carcinoma; gene therapy;
 KW rapid amplification of cDNA ends; RACE; PCR primer; ss.
 OS Homo sapiens.
 XX WO200157194-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 02-FEB-2001; 2001WO-US003471.
 XX
 XX 03-FEB-2000; 2000US-0179982P.
 PR 18-FEB-2000; 2000US-0183542P.
 PR 22-JUN-2000; 2000US-0213124P.
 PR 26-JUL-2000; 2000US-0220970P.
 PR 08-SEP-2000; 2000US-00657986.
 PR 22-SEP-2000; 2000US-0234840P.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Madison EL, Ong EO, Yeh J;
 PI
 XX WPI; 2001-488877/53.
 DR
 XX Novel single chain polypeptide comprising protease domain of type-II
 XX membrane-type serine protease or its catalytically active portion useful
 XX for treating and preventing cancer and tumor.
 PT
 XX Example 6; Page 164; 256pp; English.
 PS
 XX The invention relates to transmembrane serine proteases and their
 CC corresponding nucleotides and the protease domain of a type-II membrane-
 CC type serine protease (MTSP). MTSP is useful for identifying compounds
 CC that modulate or inhibit its proteolytic activity and for formulating a
 CC medicament for treating neoplastic disease. MTSP and its corresponding
 CC nucleotides are useful in preventing or treating tumours or cancers such
 CC as lung carcinoma, colon adenocarcinoma and ovarian carcinoma, in
 CC diagnostics and in hybridisation assays. MTSP is useful as a diagnostic
 CC marker for tumour development, growth and/or progression and as
 CC immunogens to generate antibodies that specifically bind to it. MTSP DNA
 CC is useful in a yeast two-hybrid system and in gene therapy. The present
 CC sequence is a gene-specific RACE (rapid amplification of cDNA ends) PCR
 CC primer used to obtain 5' region of cDNA encoding protease domain of MTSP1
 XX
 XX Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 17.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 30 GGAGTCCTCTGAGAGGTA 47
 Db 18 GGAGTCGTAGGAGGTA 1
 RESULT 57
 AAD36932/C
 ID AAD36932 standard; DNA; 18 BP.
 XX
 XX AAD36932;
 XX
 XX 21-AUG-2002 (first entry)
 DT
 XX Human MTSP1 protease domain cDNA amplifying sense PCR primer.
 DE
 XX Human; amide derivative; serine protease; matrilipase; MTSP1; cancer;
 KW therapy; tumour; metastasis; cytostatic; PCR; primer; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200220475-A2.
 PN
 XX 14-MAR-2002.
 PD

XX 07-SEP-2001; 2001WO-US028137.
 XX
 XX 08-SEP-2000; 2000US-00657986.
 PR
 XX (CORV-) CORVAS INT INC.
 XX
 XX Duncan DF, Madison EL, Semple JE, Coombs GS, Reiner JE, Ong EO;
 PI Araldi GL;
 XX
 XX WPI; 2002-415722/44.
 DR
 XX Amide derivatives, useful as serine protease inhibitors for reducing
 XX tumor progression and metastasis.
 PT
 XX Example 1; Page 43; 82pp; English.
 PS
 XX The invention relates to amide derivative compounds which inhibit serine
 CC protease activity of matrilipase or MTSP1. Matrilipase and MTSP1 are serine
 CC proteases reported to be expressed in high levels in certain cancer cell
 CC lines. The compounds of the invention are useful for treating conditions
 CC ameliorated by inhibition of the serine protease activity of matrilipase
 CC or MTSP1. The compounds are also useful in the prevention and treatment
 CC of cancerous conditions and decrease the growth of cancerous tumours and
 CC retard metastasis. The present sequence is a PCR primer used for
 CC amplifying human MTSP1 protease domain cDNA
 XX
 XX Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
 SQ
 Query Match 17.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 30 GGAGTCCTCTGAGAGGTA 47
 Db 18 GGAGTCGTAGGAGGTA 1
 RESULT 58
 ADA25180/C
 ID ADA25180 standard; DNA; 18 BP.
 XX
 XX ADA25180;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Human MTSP1 sense PCR primer.
 DE
 XX ss; serine protease; matrilipase; MTSP1; cancer; tumour; colon cancer;
 KW lung cancer; stomach cancer; rectal cancer; skin cancer; human;
 KW protease domain; PCR; primer.
 KW
 XX Homo sapiens.
 OS
 XX US2003050251-A1.
 PN
 XX 13-MAR-2003.
 PD
 XX 05-MAR-2002; 2002US-00092004.
 XX
 XX 08-SEP-2000; 2000US-00657986.
 PR
 XX 07-SEP-2001; 2001WO-US028137.
 PR
 XX (SEMP/) SEMPLE J E.
 PA (COOM/) COOMBS G S.
 PA (REIN/) REINER J E.
 PA (ONGE/) ONG E O.
 PA (ARAL/) ARALDI G L.
 XX
 XX Semple JE, Coombs GS, Reiner JE, Ong EO, Araldi GL;
 PI WPI; 2003-625421/59.
 XX
 XX

PT Treatment of condition ameliorated by inhibition of serine protease
 PT activity of matrilysin, e.g. cancerous tumors, retard metastasis or
 PT cancer of lung, colon and stomach, comprises administration of a peptide
 PT containing compound.
 XX
 XX
 XX Example 1; Page 14; 34pp; English.
 PS
 CC The invention relates to a method of treating a condition ameliorated by
 CC an inhibition or decrease in serine protease activity of matrilysin or
 CC MTSP1 which comprises administration of a peptide containing compound.
 CC The compound is useful for treating pathological conditions ameliorated
 CC by decreasing or inhibiting serine protease activity of matrilysin or
 CC MTSP1, for the treatment of cancerous conditions, e.g. cancerous tumors,
 CC colon cancer, lung cancer, stomach cancer, rectal cancer or skin cancer.
 CC The present sequence represents the human MTSP1 sense PCR primer.
 XX
 XX Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 17.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX

QY 30 GGAGTCCTCTGAGAGGTA 47
 DB 18 GGACTCTGAGGAGGTA 1

RESULT 59
 ADM57469/C
 ID ADM57469 standard; DNA; 18 BP.
 XX
 XX ADM57469;
 AC
 XX
 XX 03-JUN-2004 (first entry)
 DT
 XX
 XX M. tuberculosis PCR primer RD3-int-REP.R.
 DE
 XX
 XX antibacterial; vaccine; mmpL6; Mycobacterium; BCG; TbD1; ss; PCR; primer.
 KW
 XX
 XX Mycobacterium tuberculosis.
 OS
 XX
 XX BPI338657-A1.
 PN
 XX
 XX 27-AUG-2003.
 PD
 XX
 XX 25-FEB-2002; 2002EP-00290458.
 PF
 XX
 XX 25-FEB-2002; 2002EP-00290458.
 PR
 XX
 XX (INSP) INST PASTEUR.
 PA
 XX
 XX Cole S, Brosch R, Gordon S, Eiglmeier K, Garnier T;
 PI
 XX
 XX WPI; 2003-699254/67.
 DR
 XX
 XX New TbD1 nucleic acids having the mutation CTG to CGG at codon 463 of
 PT gene katG, useful for distinguishing Mycobacterium tuberculosis infection
 PT from M. africanum, M. canettii, M. microti, M. bovis, or M. bovis BCG
 PT infection.
 XX
 XX Disclosure; Page 19; 73pp; English.
 PS
 XX The invention relates to a novel isolated or purified nucleic acid. A
 CC polypeptide encoded by a nucleic acid of the invention has antibacterial
 CC activity, and may have a use in a vaccine. The nucleic acid is a TbD1
 CC nucleic acid having a fully defined sequence of 3953 bp given in the
 CC specification. The TbD1 deletion or mmpL6 551 polymorphism is useful as a
 CC genetic marker for the differentiation of Mycobacterium strain of M.
 CC tuberculosis complex. The genetic marker in association with at least one
 CC genetic markers selected from RD1, RD2, RD3, RD4, RD5, RD6, RD7, RD8,
 CC RD9, RD10, RD11, RD13, RD14, RvD1, RvD2, RvD3, RvD4, RvD5, katG463,
 CC gyrA95, oxyR285, and pncA57, may be used for the differentiation of
 CC Mycobacterium strain of M. tuberculosis complex. The nucleic acids may

CC also be used to distinguish an infection resulting from M. tuberculosis
 CC from an infection resulting from M. africanum, M. canettii, M. microti, M.
 CC bovis, M. bovis BCG. The present sequence is used in the exemplification
 CC of the invention.
 XX
 XX Sequence 18 BP; 3 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 17.1%; Score 13.2; DB 1; Length 18;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX

QY 6 AAGACGGCCTGGGATAC 23
 DB 18 AAGATCGCCTGGGGGTAC 1

RESULT 60
 ADJ82396
 ID ADJ82396 standard; DNA; 15 BP.
 XX
 XX ADJ82396;
 AC
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX
 XX KLM5Y-encoding nucleotide #124.
 DE
 XX
 XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
 KW myeloproliferative disease; blood vessel proliferative disease;
 KW angiogenesis.
 XX
 XX Synthetic.
 OS
 XX
 XX WO2003045973-A2.
 PN
 XX
 XX 05-JUN-2003.
 PD
 XX
 XX 30-SEP-2002; 2002WO-US031165.
 PF
 XX
 XX 28-NOV-2001; 2001US-0333476P.
 PR
 XX
 XX (BECT) BECTON DICKINSON & CO.
 PA (HAAL// HAALAND P D.
 PA
 XX
 XX Dean C, Heidaran M, Spargo CA;
 PI
 XX
 XX WPI; 2003-505179/47.
 DR
 XX
 XX New peptides having growth inhibitory action, useful for inhibiting tumor
 PT or cancer cell proliferation, or for treating fibrotic disorders,
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
 PT disorders.
 XX
 XX Disclosure; SEQ ID NO 177; 48pp; English.
 PS
 XX The invention relates to an isolated peptide or polypeptide (I) of no
 CC more than about 50 amino acid residues which when contacted with cells in
 CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
 CC an autocrine manner, inhibits the growth of these cells. The isolated
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
 CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
 CC muscle or bone cell. The peptides are also useful for treating fibrotic
 CC disorders, myeloproliferative diseases, and blood vessel proliferative
 CC (angiogenic) disorders. This sequence represents a possible nucleotide
 CC encoding the P3 peptide.
 XX
 XX Sequence 15 BP; 4 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
 SQ

Query Match 16.9%; Score 13; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 AGCTGATGTCCT 71
 Db 1 AGCTGATGTCCT 13

RESULT 61

ABN10031
 ID ABN10031 standard; DNA; 17 BP.

XX AC ABN10031;

XX DT 29-MAY-2002 (first entry)

XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10023.

XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 05-FEB-2001; 2001US-0266860P.

XX PA (AEOM-) AEOMICA INC.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX PF WPI; 2002-179446/23.

XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX PS Disclosure; SEQ ID NO 10023; 214pp; English.

XX CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1

CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence

XX SQ Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 16.9%; Score 13; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TCTGGAGTCTCTCT 39

Db 5 TCTGGAGTCTCTCT 17

RESULT 62

ACN73121

ID ACN73121 standard; DNA; 17 BP.

XX AC ACN73121;

XX DT 02-DEC-2004 (first entry)

XX DE Human GDMPLP-1 probe SEQ ID NO:10023.

XX KW Human; ss; probe; myosin-like protein-1; hGDMPLP-1;

XX KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;

XX KW skeletal muscle function.

XX OS Homo sapiens.

XX PN US2004137589-A1.

XX PD 15-JUL-2004.

XX PF 26-NOV-2003; 2003US-00723361.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 05-FEB-2001; 2001US-0266860P.

XX PR 25-MAY-2001; 2001US-00866108.

XX PA (GUY/) GU Y.

XX PA (JIY/) JI Y.

XX PA (PENN/) PENN S G.

XX PA (HANZ/) HANZEL D K.

XX PA (RANK/) RANK D.

XX PA (CHEN/) CHEN W.

XX PA (SHAN/) SHANNON M E.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;

XX DR WPI; 2004-533378/51.

XX PT Novel myosin-like protein-1, useful for treating or preventing disorder

PT associated with decreased expression or activity of human genome-derived
PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
function.
XX
XX Disclosure; SEQ ID NO 10023; Opp; English.
XX
XX The invention relates to a novel polypeptide (I) comprising a sequence
CC (S1) of myosin-like protein-1 (hGMDLP-1) having 2568 amino acids fully
CC defined in the specification, a fragment of at least 8 amino acids of
CC (S1), 95% deviation from (S1) which are conservative substitutions, and
CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
CC antagonist of hGMDLP-1, or as an inhibitor of hGMDLP-1 activity. A
CC pharmaceutical composition of the invention is useful for treating or
CC preventing a disorder associated with decreased expression or activity of
CC hGMDLP-1, such as a disorder of heart and/or skeletal muscle function.
CC The present sequence represents a 17-mer nucleotide, used in the
CC invention for scanning the sequence represented in ACN63103
XX
XX Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
SQ
Query Match 16.9%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 27 TCTGGAGTCTCTCT 39
Db 5 TCTGGAGTCTCTCT 17
RESULT 63
AAK35522/c
ID AAK35522 standard; cDNA; 18 BP.
AC
AC AAK35522;
XX
DT 08-JUL-1999 (first entry)
XX
XX PCR primer used to amplify 36B4 gene (in control reactions).
DE
DE Facilitative glucose transporter protein; GLUT8; malignancy;
XX breast cancer; prostate cancer; epithelial cell cancer;
KW non-insulin-dependent diabetes mellitus; insulin resistance;
KW central obesity; hypertension; dyslipidaemia; glucose intolerance;
KW cancer; 36B4 gene; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO9918125-A1.
XX
PD 15-APR-1999.
XX
XX 30-SEP-1998; 98WO-AU000819.
XX
XX 01-OCT-1997; 97AU-00009573.
XX
XX (SVIN-) ST VINCENTS INST MEDICAL RES.
PA
XX Rogers SD, Best JD;
PI
XX WPI; 1999-277253/23.
XX
XX Nucleic acid encoding a facilitative glucose transporter.
PT
XX Example 7; Page 17; 72pp; English.
XX
XX The specification describes a facilitative glucose transporter protein,
CC GLUT8, and its functional fragments. Agents that inhibit activity or
CC expression of GLUT8 (particularly non-utilizable glucose analogues,
CC antisense sequences or dominant negative mutants) are used to treat
CC malignancy, particularly cancer of breast, prostate and epithelial cells
CC (e.g. skin or colon). Agents that upregulate expression of GLUT8 (e.g.
CC the GLUT8 gene, administered by tissue-localized gene therapy) are used
CC to treat non-insulin-dependent diabetes mellitus and/or insulin

CC resistance (e.g. central obesity, hypertension, dyslipidaemia or glucose
CC intolerance). Detecting expression of GLUT8 is used for diagnosis,
CC monitoring and staging of cancers, particularly of the breast. Antibodies
CC raised against GLUT8 are useful as immunoassay reagents and as
CC therapeutic inhibitors. PCR primers AAK35521-22 were used in the course
CC of the invention
XX
XX Sequence 18 BP; 1 A; 8 C; 5 G; 4 T; 0 U; 0 Other;
SQ
Query Match 16.9%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 50 GAGCCAGCGAAGC 62
Db 14 GAGCCAGCGAAGC 2
RESULT 64
ADC04442/c
ID ADC04442 standard; DNA; 17 BP.
XX
XX ADC04442;
XX
XX 18-DEC-2003 (first entry)
DT
XX Human Na/H exchanger-like protein 1 gene oligonucleotide #889.
DE
DE ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
KW NHEPL1; passive replacement therapy; vaccine; diagnosis.
XX
XX Homo sapiens.
OS
XX EP1273660-A2.
PN
XX 08-JAN-2003.
PD
XX 25-JAN-2002; 2002BP-00001160.
PF
XX 30-JAN-2001; 2001WO-US000666.
PR
XX 23-MAY-2001; 2001US-00864761.
PR
XX 21-DEC-2001; 2001US-0343331P.
XX
XX (AEOM-) AEOMICA INC.
PA
XX Gu Y;
PI
XX WPI; 2003-302724/30.
DR
XX New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
PT passive replacement therapy or as a vaccine for treating or preventing
PT disorders associated with aberrant expression or activity of human
PT NHEPL1.
XX
XX Example 2; SEQ ID NO 929; 468pp; English.
PS
XX The invention relates to a nucleic acid molecule which encodes a Na+/H+
CC exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1
CC polypeptide, an antibody against the protein or its antigen-binding
CC fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1
CC polypeptide and an agonist are particularly useful for manufacturing a
CC medicament for treating or preventing a disorder associated with
CC decreased expression or activity of human NHEPL1. The antibody or its
CC antigen-binding fragment, and an antagonist, are useful for manufacturing
CC a medicament for treating or preventing a disorder associated with
CC increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid
CC or protein is useful as passive replacement therapy, as a vaccine, or in
CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
CC spanning the sequence of the human NHEPL1 gene (ADC03514).
XX
XX Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 16.6%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 75;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 48 AAGAGCCAGCGAGCT 63
DB 17 ATGAGCCAGCGAGAT 2

RESULT 65
ADB45336/c
ID ADB45336 standard; DNA; 17 BP.
XX AC ADB45336;
XX 18-DEC-2003 (first entry)
XX Tumour suppression/reversion associated nucleotide #5659.
DE cytostatic; antiviral; neuroprotective; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX Homo sapiens.
XX WO2003040369-A2.
PN 15-MAY-2003.
PD 17-SEP-2002; 2002WO-IB004219.
PF 17-SEP-2001; 2001PR-00011981.
PR (MOLE-) MOLECULAR ENGINES LAB.
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX Disclosure; Page 693; 771pp; French.
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 16.6%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 75;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 AAGAGCCGCTGGGAT 21

DB 17 AAGGCTGCCTGGGAT 2

RESULT 66
AAC68677/c
ID AAC68677 standard; DNA; 18 BP.
XX AC AAC68677;
XX 22-FEB-2001 (first entry)
XX Chick R35 RNA fingerprinting primer P3.
XX Chick; R35; uropathic; antiinflammatory; analgesic; gene therapy;
KW seven transmembrane receptor; neuropathic pain; inflammation;
KW incontinence; irritable bowel syndrome; RNA fingerprinting; PCR primer;
KW ss.
XX Gallus gallus.
XX WO2000064928-A2.
PN 02-NOV-2000.
PD 20-APR-2000; 2000WO-GB001546.
PF 21-APR-1999; 99GB-00009161.
PR (SMIK) SMITHKLINE BEECHAM PLC.
PA (PLAC) MAX-PLANCK INST NEUROBIOLOGY.
XX Barde Y, Friedel R, Michalovich D, Reith AD, Schnuerch H;
PI Stubbusch J;
XX WPI; 2000-679669/66.
XX Novel R35 polypeptides and polynucleotides useful for treating
PT neuropathic, inflammatory and chronic pain, incontinence and irritable
PT bowel syndrome.
XX Example 1; Page 23; 55pp; English.
XX The present sequence was used to isolate a cDNA fragment of the chick
CC seven transmembrane receptor R35 by RNA fingerprinting. R35 is useful for
CC treating neuropathic pain, inflammatory and chronic pain, incontinence,
CC and disorders of the gastrointestinal tract associated with gut motility
CC and secretion such as irritable bowel syndrome. It is also useful for
CC inducing an immune response in a mammal to protect against the diseases.
CC It is useful in screening assays to identify compounds which stimulate or
CC inhibit the function of the polypeptide, to identify membrane bound or
CC soluble receptors and also for the structure-based design of an agonist,
CC antagonist or inhibitor of R35
XX SQ Sequence 18 BP; 2 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 16.6%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 79;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACACAGCGCTGGG 18
DB 16 AACACAGCGCTGGG 1

RESULT 67
ADG14616
ID ADG14616 standard; DNA; 18 BP.
XX AC ADG14616;
XX 26-FEB-2004 (first entry)
XX

DE Human CTLA-4 exon 1 reverse PCR primer, SEQ ID NO:7.
 KW Therapeutic response; therapeutic outcome; interferon-alpha-2b;
 KW ribavirin; hepatitis C virus; HCV infection; interleukin-10;
 KW IL-10 regulatory region; single nucleotide polymorphism; SNP; haplotype;
 KW genotype; cytotoxic T-lymphocyte antigen-4; CTLA-4 promoter;
 KW CTLA-4 exon 1; bacterial infection; meningococcal infection;
 KW rheumatoid arthritis; systemic lupus erythematosus; Sjogren's syndrome;
 KW inflammatory bowel disease; multiple sclerosis; human; PCR; primer; ss.
 XX Homo sapiens.
 XX WO200268699-A1.
 XX 06-SEP-2002.
 XX 27-FEB-2002; 2002WO-US006207.
 XX 27-FEB-2001; 2001US-0271811P.
 XX (UABR-) UAB RES FOUND.
 XX Yee L, Tang J, Kaslow RA, Van Leeuwen DU;
 XX WPI; 2002-707021/76.
 XX Predicting a therapeutic response comprises comparing a first nucleic
 PT acid allele in an interleukin-10 (IL-10) regulatory region with a second
 PT nucleic acid allele in the IL-10 regulatory region associated with a
 PT known outcome.
 XX Claim 41; SEQ ID NO 7; 34pp; English.
 XX The invention relates to a method for predicting an individual's
 CC therapeutic response to the administration of interferon-alpha-2b and
 CC ribavirin for the treatment of a pathological condition, especially
 CC hepatitis C virus (HCV) infection. The method involves determining which
 CC allelic form is present at positions -3575, -2763, -1082, -819 and -592
 CC of the interleukin-10 (IL-10) regulatory region, and comparing these with
 CC the allelic forms at these positions which are associated with a known
 CC outcome of interferon-alpha-2b and ribavirin administration. Presence of
 CC the single nucleotide polymorphisms -592A and -819T, the -592A/A or -
 CC 819T/T genotypes, the combination of -592A/-819T as a haplotype,
 CC homozygosity for -592A/-819T, -592A/-819T as a genotype, or possession of
 CC the (108)TCATA haplotype (encompassing positions -3575, -2763, -1082, -
 CC 819 and -592) is associated with a sustained response to interferon-alpha
 CC -2b and ribavirin therapy. In contrast, the presence of -592C and -819C,
 CC or the (108)TCAC haplotype indicates that the patient will be non-
 CC responsive to this therapy. The method optionally further comprises
 CC detection of the allele at position -318 of the cytotoxic T-lymphocyte
 CC antigen-4 (CTLA-4) promoter and the allele at position 49 of exon 1 of
 CC the CTLA-4 gene. The invention also encompasses kits and oligonucleotide
 CC primers for use in the methods of the invention. The method and primers
 CC are useful for identifying and analyzing genetic polymorphisms in the IL-
 CC 10 regulatory region and/or cytotoxic T-lymphocyte antigen-4 which can be
 CC used in predicting an individual's response to therapeutic intervention
 CC with interferon-alpha-2b and ribavirin for HCV infection, and for
 CC predicting the responsiveness of an individual to therapy for a
 CC pathological condition, or for predicting the outcome of therapeutic
 CC intervention in pathological conditions such as bacterial infection (e.g.
 CC meningococcal infection), rheumatoid arthritis, systemic lupus
 CC erythematosus, Sjogren's syndrome, inflammatory bowel disease or multiple
 CC sclerosis. The present sequence is related to the invention.
 XX Sequence 18 BP; 7 A; 7 C; 4 G; 0 T; 0 U; 0 Other;
 XX Query Match 16.6%; Score 12.8; DB 1; Length 18;
 XX Best Local Similarity 87.5%; Pred. No. 79;
 XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 47 AAAGAGCGGCGGAGC 62
 DB 1 ACAGAGCGGCGGAGC 16
 |||||

RESULT 68
 ADL25789
 ID ADL25789 standard; DNA; 18 BP.
 XX ADL25789;
 AC ADL25789;
 XX 20-MAY-2004 (first entry)
 DT Human cancer suppressing protein associated PCR primer.
 XX ss; PCR; human; cancer suppression; cancer; primer.
 XX Homo sapiens.
 XX CN1403478-A.
 XX 19-MAR-2003.
 XX 12-SEP-2001; 2001CN-00126726.
 XX 12-SEP-2001; 2001CN-00126726.
 XX (SHAN-) SHANGHAI XINSHIJI GENE TECH DEV CO LTD.
 XX Gu J, Yang S;
 XX WPI; 2003-494227/47.
 XX Human protein with function of suppressing cancer cell growth and its
 PT coding sequence.
 XX Disclosure; Page 12; 43pp; Chinese.
 XX The invention relates to one kind of human protein with cancer
 CC suppressing function, polynucleotides encoding the polypeptide and the
 CC recombinant process of producing the polypeptide. The present invention
 CC also discloses the method of using the polypeptide in treating various
 CC diseases, such as cancer. The present invention also discloses the
 CC agonist resisting the polypeptide and its treatment effect. The present
 CC invention also discloses the application of the polynucleotides encoding
 CC the human protein with cancer suppressing function. The present sequence
 CC represents a human cancer suppressing protein associated PCR primer.
 XX Sequence 18 BP; 6 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
 XX Query Match 16.6%; Score 12.8; DB 1; Length 18;
 XX Best Local Similarity 87.5%; Pred. No. 79;
 XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 AAGACGGCGCTGGGGAT 21
 DB 3 AAGACGGCGATAGGGAT 18
 |||||

RESULT 69
 ADL74794
 ID ADL74794 standard; DNA; 18 BP.
 XX ADL74794;
 XX 16-DEC-2004 (first entry)
 DT Allele specific primer B for human stenosis marker hCV25612829.
 XX Human; ss; PCR; primer; Allele specific primer; coronary stenosis;
 KW angina; ischaemic chest pain; myocardial infarction;
 KW sudden cardiac death; SNP; single nucleotide polymorphism.
 XX Homo sapiens.
 XX WO2004081186-A2.

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XX 23-SEP-2004.
XX
XX 10-MAR-2004; 2004WO-US007140.
XX
XX 10-MAR-2003; 2003US-0453050P.
XX
XX 30-APR-2003; 2003US-0466437P.
XX
XX (APPL-) APPLERA CORP.
XX
XX Cargill M, Devlin JJ, Luke MM;
XX
XX WPI; 2004-668949/65.
XX
XX Identifying an individual who has altered risk for developing stenosis
XX comprises detecting single nucleotide polymorphism (SNP), in the
XX individual's nucleic acids.
XX
XX Claim 19; SEQ ID NO 68106; 146pp; English.
XX
XX The invention relates to identifying an individual who has altered risk
XX for developing coronary stenosis comprising detecting a single nucleotide
XX polymorphism (SNP) in any one of the 67073 nucleotide sequences (not
XX given in the specification), in the individual's nucleic acids, where the
XX presence of the SNP is correlated with an altered risk for stenosis in
XX the individual. Also included are an isolated nucleic acid molecule
XX (comprising at least 8 contiguous nucleotides where one of the
XX nucleotides is an SNP as cited above, or their complement), an isolated
XX polypeptide comprising an amino acid sequence selected from any of the
XX 696 amino acid sequences (not defined in the specification), an antibody
XX that specifically binds to the polypeptide (or its antigen-binding
XX fragment), an amplified polynucleotide containing the SNP as cited (where
XX the amplified polynucleotide is between about 16 and about 1,000
XX nucleotides in length), an isolated polynucleotide which specifically
XX hybridises to a nucleic acid molecule containing the SNP, a kit for
XX detecting a SNP in a nucleic acid, detecting a SNP in a nucleic acid
XX molecule, detecting a variant polypeptide and identifying an agent useful
XX in therapeutically or prophylactically treating stenosis. The detection
XX step of the method is carried out by a process selected from allele-
XX specific probe hybridisation, allele-specific primer extension, allele-
XX specific amplification, sequencing, 5' nuclease digestion, molecular
XX beacon assay, oligonucleotide ligation assay, size analysis, and single-
XX stranded conformation polymorphism. The method is useful for identifying
XX an individual who has altered risk for developing coronary stenosis,
XX which can lead to angina (ischaemic chest pain), myocardial infarction
XX and ultimately sudden cardiac death. The present sequence is an allele
XX specific primer for amplifying a SNP-containing region of a human marker
XX gene associated with stenosis. NOTE: SEQ ID 1-67771 are not shown in the
XX specification but are provided on a CD-R named CL001510CDR which was not
XX supplied with the specification.
XX
XX Sequence 18 BP; 5 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 16.6%; Score 12.8; DB 1; Length 18;
XX Best Local Similarity 87.5%; Pred. No. 79;
XX Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 56 GCGAAGCTGATGTCCT 71
Db 3 GCCAAGATGATGTCCT 18
XX
RESULT 70
ADV37028
ID ADV37028 standard; RNA; 15 BP.
XX
XX ADV37028;
XX
XX 10-FEB-2005 (first entry)
XX
XX Human anti-HER2 NCH ribozyme substrate sequence #907.
XX
XX Enzymatic nucleic acid molecule; gene expression; down regulation;

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```

KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyze; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX
XX Homo sapiens.
XX
XX WO200116312-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
XX
XX 27-SEP-1999; 99US-00406643.
XX
XX 27-SEP-1999; 99US-0156236P.
XX
XX 27-SEP-1999; 99US-0156467P.
XX
XX 08-NOV-1999; 99US-00436430.
XX
XX 06-DEC-1999; 99US-0169100P.
XX
XX 29-DEC-1999; 99US-00474432.
XX
XX 29-DEC-1999; 99US-0173612P.
XX
XX 30-DEC-1999; 99US-00476387.
XX
XX 04-FEB-2000; 2000US-00498824.
XX
XX 20-MAR-2000; 2000US-00531025.
XX
XX 14-APR-2000; 2000US-0197769P.
XX
XX 23-MAY-2000; 2000US-00578223.
XX
XX 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Meswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX Karpaisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX obesity and heart disease.
XX
XX Example 7; Page 490; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
XX molecules (e.g. ribozymes) to modulate gene expression. The invention
XX also methods for their use to down regulate or inhibit the expression of
XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine C
XX aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX nucleic acid molecules used to inhibit the expression of the said genes
XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyze,
XX zinzyme, and/or DNazyme motifs. The methods of the invention are useful
XX for treating cancer, in particular breast cancer, Alzheimer's disease,
XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX diseases, hepatitis B infections, and hepatitis and hepatocellular
XX carcinoma. The enzymatic nucleic acid molecules can also be used as
XX diagnostic tools to examine genetic drift and mutations within diseased
XX cells and to detect the presence of specific RNA in a cell. The present
XX sequence represents a substrate/target sequence for an anti-HER2 NCH
XX ribozyme used in the examples of the present invention. Note: Some SEQ ID
XX Nos are repeated more than once in the specification, but these have
XX different sequences associated with them.
XX
XX Sequence 15 BP; 3 A; 5 C; 4 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 16.1%; Score 12.4; DB 1; Length 15;
XX Best Local Similarity 71.4%; Pred. No. 75;

```

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCTCTGA 41
|:||||| |:|

Db 1 CUGGAGCCUCUGA 14

RESULT 71
ADV64524
ID ADV64524 standard; RNA; 17 BP.

CC AC ADV64524;

CC XX 10-FEB-2005 (first entry)

CC DE Human Her2 class II (zincyme) ribozyme substrate sequence #506.

CC KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW C-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyne; zincyme; DNzyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.

CC OS Homo sapiens.

CC XX WO200116312-A2.

CC XX 08-MAR-2001.

CC XX 30-AUG-2000; 2000WO-US023998.

CC PR 31-AUG-1999; 99US-0151713P.

CC PR 27-SEP-1999; 99US-00406643.

CC PR 27-SEP-1999; 99US-0156236P.

CC PR 27-SEP-1999; 99US-0156467P.

CC PR 08-NOV-1999; 99US-00436430.

CC PR 08-DEC-1999; 99US-0169100P.

CC PR 29-DEC-1999; 99US-00474432.

CC PR 29-DEC-1999; 99US-0173612P.

CC PR 30-DEC-1999; 99US-00476387.

CC PR 04-FEB-2000; 2000US-00498824.

CC PR 20-MAR-2000; 2000US-00531025.

CC PR 14-APR-2000; 2000US-0197769P.

CC PR 23-MAY-2000; 2000US-00578223.

CC PR 09-AUG-2000; 2000US-00636385.

CC PA (RIBO-) RIBOZYME PHARM INC.

CC XX Meswiggen J, Uman N, Blatt L, Beigelman L, Burgin A;
PI Karpinsky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
CC WPI; 2001-244406/25.

CC XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.

CC XX Example 16; Page 633; 717pp; English.

CC CC The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic

CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyne,
CC zincyme, and/or DNzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.

CC SQ Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 71.4%; Pred. No. 86;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 28 CTGGAGTCTCTGA 41

|:||||| |:|

Db 4 CUGGAGCCUCUGA 17

RESULT 72

ABN10037

ID ABN10037 standard; DNA; 17 BP.

CC AC ABN10037;

CC XX 29-MAY-2002 (first entry)

CC DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10029.

CC KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;

CC KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

CC KW skeletal muscle disorder; amplicon; screening; ss.

CC OS Homo sapiens.

CC XX WO200192524-A2.

CC XX 06-DEC-2001.

CC XX 25-MAY-2001; 2001WO-US016981.

CC PR 26-MAY-2000; 2000US-0207456P.

CC PR 21-SEP-2000; 2000US-0234687P.

CC PR 27-SEP-2000; 2000US-0236359P.

CC PR 04-OCT-2000; 2000GB-00024263.

CC PR 30-JAN-2001; 2001WO-US000661.

CC PR 30-JAN-2001; 2001WO-US000662.

CC PR 30-JAN-2001; 2001WO-US000663.

CC PR 30-JAN-2001; 2001WO-US000664.

CC PR 30-JAN-2001; 2001WO-US000665.

CC PR 30-JAN-2001; 2001WO-US000666.

CC PR 30-JAN-2001; 2001WO-US000667.

CC PR 30-JAN-2001; 2001WO-US000668.

CC PR 30-JAN-2001; 2001WO-US000669.

CC PR 30-JAN-2001; 2001WO-US000670.

CC PR 05-FEB-2001; 2001US-0266860P.

CC XX (AEOM-) AEOMICA INC.

CC XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

CC XX WPI; 2002-179446/23.

CC XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,

CC PT or as specific biomolecule capture probes for surface-enhanced laser

CC PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

CC XX

PS Disclosure; SEQ ID NO 10029; 214pp; English.

XX The present invention describes a human genome-derived myosin-like

CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-1

CC can be used in gene therapy and vaccine production. The hGDMLP-1

CC nucleic acids can be used as probes to detect, characterise and quantify

CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMLP-1

CC protein variants having desired phenotypic improvements, and for

CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be

CC used as immunogens to raise antibodies that specifically recognise hGDMLP

CC -1 proteins, as standards in assays used to determine the concentration

CC and/or amount specifically of hGDMLP proteins, as specific biomolecule

CC capture probes for surface-enhanced laser desorption/ionisation, as

CC therapeutic supplement in patients having specific deficiency in hGDMLP-1

CC production, and in vaccines or for replacement therapy. The

CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a

CC disorder associated with the expression of hGDMLP-1, in particular heart

CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the

CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequence

XX

SQ Sequence 17 BP; 2 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 86;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 29 TGGAGTCTCTGAG 42

DB 1 TGGAGTCTCTG 14

RESULT 73

ID ABZ65329

XX ABZ65329 standard; RNA; 17 BP.

AC ABZ65329;

XX

DT 21-MAR-2003 (first entry)

DE Human HER2 DNAzyme substrate #786.

XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;

KW anti-rheumatic; cancer; AIDS; ss.

XX Homo sapiens.

OS

XX WO200297114-A2.

PN

XX

PD 05-DEC-2002.

XX

PF 29-MAY-2002; 2002WO-US016840.

XX

PR 29-MAY-2001; 2001US-0294140P.

PR 05-JUN-2001; 2001US-0296249P.

PR 10-SEP-2001; 2001US-0318471P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX

PI Mcswiggen J;

XX

XX WPI; 2003-140484/13.

XX

PT Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding

PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX

PS Claim 4; Page 148; 185pp; English.

XX The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates

CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-

CC rheumatic activity. The nucleic acid molecules are useful for reducing

CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are

CC also useful for treating breast, ovarian, colorectal, lung, prostate,

CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences

CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,

CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human

CC ribozymes of the invention

XX

SQ Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;

Best Local Similarity 71.4%; Pred. No. 86;

Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 28 CTGGAGTCTCTGCA 41

DB 4 CUGAGCCUCUGA 17

RESULT 74

ADC04446/C

ID ADC04446 standard; DNA; 17 BP.

XX

AC ADC04446;

XX

DT 18-DEC-2003 (first entry)

DE Human Na/H exchanger-like protein 1 gene oligonucleotide #893.

XX

XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;

KW NHEP1; passive replacement therapy; vaccine; diagnosis.

KW Homo sapiens.

OS

XX BP1273660-A2.

PN

XX

PD 08-JAN-2003.

XX

PF 25-JAN-2002; 2002EP-00001160.

XX

PR 30-JAN-2001; 2001WO-US000666.

PR 23-MAY-2001; 2001US-00864761.

PR 21-DEC-2001; 2001US-0343331P.

XX

PA (ABOM-) AEOMICA INC.

XX

XX Gu Y;

PI

XX

DR WPI; 2003-302724/30.

XX

PT New human sodium-hydrogen exchanger like protein 1 (NHEP1), useful as a

PT passive replacement therapy or as a vaccine for treating or preventing

PT disorders associated with aberrant expression or activity of human

PT NHEP1.

XX

PS Example 2; SEQ ID NO 933; 468pp; English.

XX

CC The invention relates to a nucleic acid molecule which encodes a Na+/H+

CC exchanger like protein (NHEP1). The NHEP1 nucleic acid molecule, NHEP1

CC polypeptide, an antibody against the protein or its antigen-binding

CC fragment is useful in therapy. The NHEP1 nucleic acid molecule, NHEP1

CC polypeptide and an agonist are particularly useful for manufacturing a

CC medicament for treating or preventing a disorder associated with

CC decreased expression or activity of human NHEP1. The antibody or its

CC antigen-binding fragment, and an antagonist, are useful for manufacturing

CC a medicament for treating or preventing a disorder associated with

CC increased expression or activity of human NHEP1. The NHEP1 nucleic acid

CC or protein is useful as passive replacement therapy, as a vaccine, or in
 CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
 CC spanning the sequence of the human NHEPL1 gene (ADC03514).

XX Sequence 17 BP; 1 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 86;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 47 AAGAGCCAGCGAA 60
 Db 14 AATGAGCCAGCGAA 1

RESULT 75

ADC04441/c
 ID ADC04441 standard; DNA; 17 BP.

XX AC ADC04441;

XX DT 18-DEC-2003 (first entry)

XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #888.

XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
 KW NHEPL1; passive replacement therapy; vaccine; diagnosis.

XX OS Homo sapiens.

XX PN EP1273660-A2.

XX PD 08-JAN-2003.

XX PF 25-JAN-2002; 2002EP-00001160.

XX PR 30-JAN-2001; 2001WO-US000866.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 21-DEC-2001; 2001US-0343331P.

XX PA (ABOM-) ABOMICA INC.

XX PI Gu Y;

XX WPI; 2003-302724/30.

XX PT New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
 PT passive replacement therapy or as a vaccine for treating or preventing
 PT disorders associated with aberrant expression or activity of human
 PT NHEPL1.

XX Example 2; SEQ ID NO 928; 468pp; English.

XX The invention relates to a nucleic acid molecule which encodes a Na+/H+
 CC exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1
 CC polypeptide, an antibody against the protein or its antigen-binding
 CC fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1
 CC polypeptide and an agonist are particularly useful for manufacturing a
 CC medicament for treating or preventing a disorder associated with
 CC decreased expression or activity of human NHEPL1. The antibody or its
 CC antigen-binding fragment, and an antagonist, are useful for manufacturing
 CC a medicament for treating or preventing a disorder associated with
 CC increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid
 CC or protein is useful as passive replacement therapy, as a vaccine, or in
 CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
 CC spanning the sequence of the human NHEPL1 gene (ADC03514).

XX Sequence 17 BP; 3 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match

Best Local Similarity 16.1%; Score 12.4; DB 1; Length 17;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAAGCT 63
 Db 16 GAGCCAGCGAAGAT 3

RESULT 76

ADC04440/c
 ID ADC04440 standard; DNA; 17 BP.

XX AC ADC04440;

XX DT 18-DEC-2003 (first entry)

XX DE Human Na/H exchanger-like protein 1 gene oligonucleotide #887.

XX ss; gene therapy; vaccine; sodium/hydrogen exchanger like protein;
 KW NHEPL1; passive replacement therapy; vaccine; diagnosis.

XX OS Homo sapiens.

XX PN EP1273660-A2.

XX PD 08-JAN-2003.

XX PF 25-JAN-2002; 2002EP-00001160.

XX PR 30-JAN-2001; 2001WO-US000866.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 21-DEC-2001; 2001US-0343331P.

XX PA (ABOM-) ABOMICA INC.

XX PI Gu Y;

XX WPI; 2003-302724/30.

XX PT New human sodium-hydrogen exchanger like protein 1 (NHEPL1), useful as a
 PT passive replacement therapy or as a vaccine for treating or preventing
 PT disorders associated with aberrant expression or activity of human
 PT NHEPL1.

XX Example 2; SEQ ID NO 927; 468pp; English.

XX The invention relates to a nucleic acid molecule which encodes a Na+/H+
 CC exchanger like protein (NHEPL1). The NHEPL1 nucleic acid molecule, NHEPL1
 CC polypeptide, an antibody against the protein or its antigen-binding
 CC fragment is useful in therapy. The NHEPL1 nucleic acid molecule, NHEPL1
 CC polypeptide and an agonist are particularly useful for manufacturing a
 CC medicament for treating or preventing a disorder associated with
 CC decreased expression or activity of human NHEPL1. The antibody or its
 CC antigen-binding fragment, and an antagonist, are useful for manufacturing
 CC a medicament for treating or preventing a disorder associated with
 CC increased expression or activity of human NHEPL1. The NHEPL1 nucleic acid
 CC or protein is useful as passive replacement therapy, as a vaccine, or in
 CC diagnostic methods. This sequence corresponds to a 17-mer oligonucleotide
 CC spanning the sequence of the human NHEPL1 gene (ADC03514).

XX Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match

Best Local Similarity 16.1%; Score 12.4; DB 1; Length 17;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 50 GAGCCAGCGAAGCT 63
 Db 17 GAGCCAGCGAAGAT 4

RESULT 77

ADI47813
 ID ADI47813 standard; DNA; 17 BP.

XX AC ADI47813;

XX 15-APR-2004 (first entry)
 XX Human tumour suppression/reversion-related DNA sequence SeqID316.
 DE
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
 KW primer; PCR; gene chip; antisense; viral disease; tumour;
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
 XX
 OS Homo sapiens.
 XX
 XX WO2003025177-A2.
 XX
 XX 27-MAR-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004523.
 XX
 XX 17-SEP-2001; 2001FR-00011980.
 XX
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX
 XX Teleman A, Anson R, Tuijnder M;
 PI
 XX WPI; 2003-313354/30.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX Disclosure; SEQ ID NO 316; 30pp; French.
 PS
 XX This invention relates to novel isolated nucleic acid sequences involved
 CC in the phenomena of tumour suppression, tumour reversion, apoptosis
 CC and/or resistance to viruses. The invention may be useful for the
 CC development of compounds with a cytostatic, virucide, neuroprotective,
 CC nootropic or neuroleptic activity. The DNA sequences may be useful as
 CC probes and primers for detecting, identifying, quantifying and/or
 CC amplifying nucleic acid, for example as one component of a gene chip, in
 CC vitro as antisense reagents and for production of recombinant
 CC polypeptides. The invention may therefore be useful for preparation of
 CC pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia. The
 CC present sequence is that of a nucleic acid sequence of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences
 XX
 XX Sequence 17 BP; 1 A; 4 C; 6 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 16.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 86;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 27 TCTGGAGTCTCTG 40
 Db ||||| |||||
 3 TCTGGTGTCTCTG 16
 RESULT 78
 AEB58478
 ID AEB58478 standard; mRNA; 17 BP.
 XX
 AC AEB58478;
 XX
 XX 22-SEP-2005 (first entry)
 DT
 XX Human VEGF receptor 1 (flt-1) DNAzyme target sequence SEQ ID 1056.
 DE
 XX VEGF receptor; angiogenesis; cancer; tumor; ocular disease;
 KW diabetic retinopathy; age related macular degeneration;
 KW angiogenesis disorder; rheumatoid arthritis; psoriasis; wound healing;

KW endometriosis; endometroid carcinoma; gynecological bleeding disorder;
 KW mensturation disorder; premenstrual syndrome; menopause; Gynecological;
 KW Cytostatic; Ophthalmological; Antidiabetic; Antiangiogenic;
 KW Antipsoriatic; Antirheumatic; Antiarthritic; Vulnerary; Hemostatic;
 KW Contraceptive; ss; enzymatic nucleic acid.
 XX
 OS Homo sapiens.
 XX
 XX WO200296927-A2.
 XX
 XX 05-DEC-2002.
 XX
 XX 29-MAY-2002; 2002WO-US017674.
 XX
 XX 29-MAY-2001; 2001US-00870161.
 XX
 XX 30-NOV-2001; 2001US-0334461P.
 XX
 XX 03-MAY-2002; 2002US-00138674.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX (CHIR) CHIRON CORP.
 PA
 XX Escobedo J, Mcswiggen J, Pavco P, Stinchcomb D, Sandberg J;
 PI Gordon G;
 PI
 XX WPI; 2003-140439/13.
 XX
 XX Novel enzymatic nucleic acids, ribozymes, which modulate expression of
 PT genes encoding vascular endothelial growth factor and/or VEGF receptor,
 PT useful for inhibiting tumor angiogenesis in cell, and for treating
 PT cancer.
 XX
 XX Disclosure; SEQ ID NO 1056; 172pp; English.
 PS
 XX The invention relates to enzymatic nucleic acids (I) i.e.
 CC ribozymes/DNAzymes/Zinzymes that target and modulate expression of, genes
 CC encoding vascular endothelial growth factor (VEGF) and/or VEGF receptor
 CC (VEGFR1 and 2 encode by the Flt-1 and Kdr genes respectively). Also
 CC included are a composition comprising (I) and a carrier, administering
 CC (I) to a cell (by contacting the cell with the compound under conditions
 CC suitable for the administration), administering (I) to a cell (in
 CC conjunction with one or more other drug by contacting the cell with the
 CC compound and the other drug under conditions suitable for the
 CC administration), administering (I) to a mammal (by contacting the mammal
 CC with the compound under conditions suitable for the administration),
 CC treating (M1) a subject having endometriosis (by contacting a subject
 CC with, or administering to subject, a nucleic acid molecule (II) that
 CC modulates expression of VEGF, VEGFR1, and/or VEGFR2), a mammalian cell
 CC (III) comprising (I) and administering to a mammal (I) (in conjunction
 CC with a chemotherapeutic agent comprising contacting the mammal with the
 CC compound and the chemotherapeutic agent under conditions suitable for the
 CC administration). (I) is administered to a mammalian cell, preferably
 CC human cell in the presence of a delivery reagent which is a lipid such as
 CC cationic lipid or phospholipid, or a liposome. The enzymatic nucleic acid
 CC molecule has an endonuclease activity to cleave RNA encoded by an VEGFR1
 CC and/or VEGFR2 gene, and is in a hammerhead, inozyme, DNAzyme, G-cleaver,
 CC or Amberzyme configuration. The enzymatic nucleic acids are useful for
 CC inhibiting ocular angiogenesis associated with diabetic retinopathy or
 CC age-related diabetic retinopathy, in a subject. They are also useful for
 CC inhibiting angiogenesis, preferably tumor angiogenesis in cell, and for
 CC treating a subject having a condition associated with an increased level
 CC of VEGF receptor, where the condition is cancer, e.g. breast cancer, lung
 CC cancer (such as non-small cell lung carcinoma), colorectal cancer, renal
 CC cancer (such as renal cell carcinoma), pancreatic cancer. The enzymatic
 CC nucleic acids are useful for treating a subject (preferably human) having
 CC endometriosis, psoriasis, age-related macular degeneration, proliferative
 CC diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis,
 CC wound healing, endometrial carcinoma, gynecological bleeding disorders,
 CC irregular menstrual cycles, ovulation, premenstrual syndrome, and
 CC menopausal dysfunction. The enzymatic nucleic acids are useful for birth
 CC control by inhibiting ovulation or embryonic uterine implantation. The
 CC present sequence is a target sequence from the human VEGFR1/flt-1 mRNA.
 XX
 XX Sequence 17 BP; 2 A; 5 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 64.3%; Pred. No. 86;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 26 CTCCTGGAGTCTCT 39
 Db 2 CUCGGAGUCCUCU 15

RESULT 79
 ACN73127
 ID ACN73127 standard; DNA; 17 BP.
 XX AC
 AC AC
 XX AC
 XX AC
 DT 02-DEC-2004 (first entry)
 DE Human GDMPLP-1 probe SEQ ID NO:10029.
 XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;
 KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.
 XX Homo sapiens.
 OS Homo sapiens.
 XX US2004137589-A1.
 XX 15-JUL-2004.
 XX 26-NOV-2003; 2003US-00723361.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001WO-US000670.
 PR 25-MAY-2001; 2001US-0266860P.
 XX (GUY/) GU Y.
 PA (JTY/) JI Y.
 PA (PENN/) PENN S G.
 PA (HANK/) HANZEL D K.
 PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;
 WPI; 2004-533378/51.
 XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.
 XX Disclosure; SEQ ID NO 10029; Opp; English.
 XX (S1) of myosin-like protein-1 (hGDMPLP-1) comprising a sequence
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or

CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103
 XX

QY 29 TGGAGTCTCTGAG 42
 Db 1 TGGAGTCTCTGTG 14

Query Match 16.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 86;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 80
 ADX59138
 ID ADX59138 standard; DNA; 17 BP.
 XX AC
 AC ADX59138;
 XX 21-APR-2005 (first entry)
 DT Human liver cancer-associated gene promoter-related PCR primer SeqID107.
 XX DNA methylation; promoter; liver tumor; PCR; primer; ss.
 KW Homo sapiens.
 OS Homo sapiens.
 XX CN1451759-A.
 XX 29-OCT-2003.
 XX 15-APR-2002; 2002CN-00111351.
 XX 15-APR-2002; 2002CN-00111351.
 XX (SHAN-) SHANGHAI INST ONCOLOGY.
 XX Zhu J;
 WPI; 2004-110093/12.
 XX Methylation state of liver cancer related gene promoter CpG island and
 PT its use in detecting liver cancer.
 XX Claim 5; SEQ ID NO 107; 38pp; Chinese.
 XX This invention relates to novel methylation state information about CpG
 CC islands in the promoter region of a gene associated with primary liver
 CC cancer, its use and a reagent kit for detecting primary liver cancer. The
 CC reagent kit contains a methylation-specific restriction endonuclease and
 CC the promoter CpG island-specific primer pairs of a gene associated with
 CC liver cancer, a reagent for transforming the methylation cytosine to
 CC uracil and primers for the promoter CpG island of the gene associated
 CC with liver cancer. The present sequence is that of a PCR primer which was
 CC for amplification of a region of a human liver cancer-associated gene
 CC promoter during the analysis of methylation state in the exemplification
 CC of the invention.
 XX Sequence 17 BP; 7 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 16.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 86;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 49 AGAGCCAGCGAAGC 62
 Db 2 AAAGCCAGCGAAGC 15

RESULT 81
ADZ34403
ID ADZ34403 standard; RNA; 17 BP.
XX
XX
AC ADZ34403;
XX
XX 30-JUN-2005 (first entry)
XX
XX Human HER2 substrate RNA sequence SEQ ID NO:5441.
DE
XX short interfering RNA; siRNA; RNA interference; gene silencing;
KW cytosolic; cancer; HER2; substrate; ss.
XX
XX Homo sapiens.
XX
XX US2005080031-A1.
XX
XX 14-APR-2005.
XX
XX 26-NOV-2003; 2003US-00724270.
XX
XX 18-MAY-2001; 2001US-0292217P.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX
XX 06-JUN-2001; 2001US-0296249P.
XX
XX 20-JUL-2001; 2001US-0306883P.
XX
XX 13-AUG-2001; 2001US-0311865P.
XX
XX 10-SEP-2001; 2001US-0318471P.
XX
XX 20-FEB-2002; 2002US-0358580P.
XX
XX 06-MAR-2002; 2002US-0362016P.
XX
XX 11-MAY-2002; 2002US-0363124P.
XX
XX 20-MAY-2002; 2002WO-US015876.
XX
XX 29-MAY-2002; 2002US-00157580.
XX
XX 08-JUN-2002; 2002US-00163552.
XX
XX 06-JUN-2002; 2002US-0386782P.
XX
XX 23-AUG-2002; 2002US-0406784P.
XX
XX 05-SEP-2002; 2002US-0408378P.
XX
XX 09-SEP-2002; 2002US-0409293P.
XX
XX 10-SEP-2002; 2002US-00238700.
XX
XX 15-JAN-2003; 2003US-0440129P.
XX
XX 20-FEB-2003; 2003WO-US005028.
XX
XX 20-FEB-2003; 2003WO-US005346.
XX
XX 16-APR-2003; 2003US-00417012.
XX
XX 24-APR-2003; 2003US-00422704.
XX
XX 30-APR-2003; 2003US-00427160.
XX
XX 23-MAY-2003; 2003US-00444853.
XX
XX 29-AUG-2003; 2003US-00652791.
XX
XX 23-OCT-2003; 2003US-00693059.
XX
XX (SIRN-) SIRNA THERAPEUTICS INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2005-331166/34.
XX
XX Novel double-stranded short interfering RNA molecule having first
PT nucleotide sequence complementary to RNA encoding HER2 or its portion,
PT and second nucleotide sequence having complementarity to first sequence,
PT useful for treating cancer.
XX
XX Example 10; SEQ ID NO 5441; 143pp; English.
XX
XX The invention relates to a double-stranded short interfering RNA (siRNA)
CC molecule (I) comprising a first nucleotide sequence having 19-23
CC nucleotides complementary to an RNA sequence encoding HER2 or its
CC portion, and a second nucleotide sequence having 19-23 nucleotides
CC exhibiting complementarity to the first sequence, and including at least
CC one nucleotide that is not a 2'-OH containing ribonucleotide. Also
CC described is a method of producing a class of nucleic acid-based gene
CC modulating agents that exhibit a high degree of specificity for RNA of a
CC desired target. (I) is useful for modulating HER2 activity in a cell, and
CC for treating diseases or conditions related to levels of HER2 gene

CC expression. (I) is useful for treating cancer, such as pancreatic cancer,
CC bladder cancer, lung cancer, breast cancer or prostate cancer. The
CC present sequence represents a human HER2 substrate RNA sequence for a
CC DNzyme (ribozyme), which is used in an example from the present
CC invention for the identification of potential target sites in human HER2
CC RNA.
XX
XX Sequence 17 BP; 2 A; 5 C; 7 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 16.1%; Score 12.4; DB 1; Length 17;
XX Best Local Similarity 71.4%; Pred.No. 86;
XX Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 28 CTGGAGTCTCTCGA 41
|:||||| |:|:
DB 4 CUGGAGCCCUUGA 17
RESULT 82
AAA23004/C
ID AAA23004 standard; RNA; 17 BP.
XX
XX AAA23004;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6230.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Oslar-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX WO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factors.
XX
XX Claim 54; Page 256; 305pp; English.
XX
XX The present invention describes enzymatic cleavage of nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to

AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ARNT, integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Oster-Weber-Rendu syndrome, and other syndromes and diseases related to the levels of ARNT, Tie-2, integrin subunit alpha-6, or integrin subunit beta-3

Sequence 17 BP; 5 A; 7 C; 2 G; 0 T; 3 U; 0 Other;

Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 92;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 16 GGGGATACAACTCTGGGA 32
Db 17 GGGGGTATTACTCTGGGA 1

RESULT 83

ADV05926

ID ADV05926 standard; RNA; 17 BP.

XX AC ADV05926;

XX DT 10-FEB-2005 (first entry)

XX DE Human BACE DNazyme substrate sequence #192.

XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX KW c-erbB; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX KW amberyne; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
XX KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX KW ss.

XX OS Homo sapiens.

XX PN WO200116312-A2.

XX PD 08-MAR-2001.

XX PF 30-AUG-2000; 2000WO-US023998.

XX PR 31-AUG-1999; 99US-0151713P.

XX PR 27-SEP-1999; 99US-00406643.

XX PR 27-SEP-1999; 99US-0156236P.

XX PR 27-SEP-1999; 99US-0156467P.

XX PR 08-NOV-1999; 99US-00436430.

XX PR 06-DEC-1999; 99US-0169100P.

XX PR 29-DEC-1999; 99US-00474432.

XX PR 29-DEC-1999; 99US-0173612P.

XX PR 30-DEC-1999; 99US-00476387.

XX PR 04-FEB-2000; 2000US-00498824.

XX PR 20-MAR-2000; 2000US-00531025.

XX PR 14-APR-2000; 2000US-0197769P.

XX PR 23-MAY-2000; 2000US-00578223.

XX PR 09-AUG-2000; 2000US-00636385.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
XX PI Karpelesky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;

WPI; 2001-244406/25.

Enzymatic nucleic acid molecules able to cleave separate RNA molecules are used for treating cancer, Alzheimer's disease, hepatitis, diabetes, obesity and heart disease.

Example 4; Page 380; 717pp; English.

The present invention relates to the use of enzymatic nucleic acid molecules (e.g. ribozymes) to modulate gene expression. The invention also methods for their use to down regulate or inhibit the expression of genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1), presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic nucleic acid molecules used to inhibit the expression of the said genes include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyne, zinzyme, and/or DNazyme motifs. The methods of the invention are useful for treating cancer, in particular breast cancer, Alzheimer's disease, diabetes, obesity, cardiac diseases e.g. heart disease, age-related diseases, hepatitis B infections, and hepatitis and hepatocellular carcinoma. The enzymatic nucleic acid molecules can also be used as diagnostic tools to examine genetic drift and mutations within diseased cells and to detect the presence of specific RNA in a cell. The present sequence represents a substrate/target sequence for a DNazyme used in the examples of the present invention. Note: Some SEQ ID Nos are repeated more than once in the specification, but these have different sequences associated with them.

Sequence 17 BP; 2 A; 3 C; 8 G; 0 T; 4 U; 0 Other;

Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 92;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 61 GCTGATGCTCTGTCAAG 77
Db 1 GCTGUGUGUCGCGCAAG 17

RESULT 84

ADV05024

ID ADV05024 standard; RNA; 17 BP.

XX AC ADV05024;

XX DT 10-FEB-2005 (first entry)

XX DE Human BACE zinzyme ribozyme substrate sequence #68.

XX KW Enzymatic nucleic acid molecule; gene expression; down regulation;
XX KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX KW c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX KW amberyne; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
XX KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX KW ss.

XX OS Homo sapiens.

XX PN WO200116312-A2.

XX PD 08-MAR-2001.

XX PF 30-AUG-2000; 2000WO-US023998.

XX PR 31-AUG-1999; 99US-0151713P.

XX PR 27-SEP-1999; 99US-00406643.

XX PR 27-SEP-1999; 99US-0156236P.

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PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 28-DEC-1999; 99US-00474432.
PR 28-DEC-1999; 99US-0073612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpiskiy A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
XX Example 4; Page 371; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention of
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
CC zinzyme, and/or DNazyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.
XX
XX Sequence 17 BP; 2 A; 3 C; 8 G; 0 T; 4 U; 0 Other;
SQ
Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 92;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 61 GCTGATGCTCTGTCGAAG 77
Db 1 CGUGUGUGUGGCGAAG 17
RESULT 85
ADV04194
ID ADV04194 standard; RNA; 17 BP.
XX
XX ADV04194;
AC
XX
XX 10-FEB-2005 (first entry)
DT
XX
XX Human BACE G-cleaver ribozyme substrate sequence #97.
XX
XX Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;

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KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberzyme; zinzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX
XX Homo sapiens.
XX
XX WO200116312-A2.
XX
XX 08-MAR-2001.
XX
XX 30-AUG-2000; 2000WO-US023998.
XX
XX 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 27-SEP-1999; 99US-0156467P.
PR 08-NOV-1999; 99US-00436430.
PR 06-DEC-1999; 99US-0169100P.
PR 28-DEC-1999; 99US-00474432.
PR 28-DEC-1999; 99US-0073612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpiskiy A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
XX
XX WPI; 2001-244406/25.
XX
XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
PT obesity and heart disease.
XX
XX Example 4; Page 366; 717pp; English.
XX
XX The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention of
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
CC zinzyme, and/or DNazyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for a ribozyme used in
CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
CC more than once in the specification, but these have different sequences
CC associated with them.
XX
XX Sequence 17 BP; 2 A; 3 C; 8 G; 0 T; 4 U; 0 Other;
SQ
Query Match 15.8%; Score 12.2; DB 1; Length 17;
Best Local Similarity 58.8%; Pred. No. 92;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 61 GCTGATGCTCTGTCGAAG 77

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CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX SQ Sequence 17 BP; 6 A; 2 C; 8 G; 0 T; 1 U; 0 Other;
 Query Match 15.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 76.5%; Pred. No. 92;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 GACGGCCTGGGGATACA 24
 || |||||
 Db 1 GAAGGCCUGGGAAAGA 17

RESULT 88
 ACN11559/c
 ID ACN11559 standard; RNA; 17 BP.
 XX ACN11559;
 XX 22-APR-2004 (first entry)
 XX WNV minus strand Inozyme substrate SEQ ID NO 11562.
 XX WNV; West Nile Virus; antiinflammatory; cytotstatic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX West Nile Virus.
 OS
 XX
 PN WO200268637-A2.
 XX
 XX 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-USO48350.
 XX 20-OCT-2000; 2000US-0242411P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI WPI; 2002-706994/76.
 XX
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (WNV), useful for treating a condition related to WNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 11562; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
 CC treating a condition related to WNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
 CC nucleic acid molecules further comprise at least five ribose residues, at
 CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
 CC least three of the 5' terminal nucleotides and a 3' end modification of a
 CC 3'-3', inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
 CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
 CC in the specification. The present sequence is that of a nucleic acid
 CC molecule of the invention

XX SQ Sequence 17 BP; 1 A; 8 C; 2 G; 0 T; 6 U; 0 Other;
 Query Match 15.8%; Score 12.2; DB 1; Length 17;

Best Local Similarity 82.4%; Pred. No. 92;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 GACGGCCTGGGGATACA 24
 || |||||
 Db 17 GAAGGCCUGGGAAAGA 1

RESULT 89
 ACA09006/c
 ID ACA09006 standard; RNA; 17 BP.
 XX ACA09006;
 XX 03-JUN-2003 (first entry)
 XX NFKB sub-unit modulating amberzyme substrate #169.
 XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX Homo sapiens.
 OS
 XX US2002177568-A1.
 XX 28-NOV-2002.
 XX 23-MAY-2001; 2001US-00864785.
 XX 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-00777916.
 XX (STIN/) STINCHOMB D T.
 PA (MCSW/) MCSWIGGEN J.
 PA (DRAP/) DRAPER K G.
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 PI WPI; 2003-340953/32.
 XX
 XX Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX
 XX Claim 3; Page 53; 72pp; English.
 XX
 XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,

CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule

XX
 SQ Sequence 17 BP; 2 A; 9 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 15.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 92;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 AAGAGCGCGCTGGGATA 22
 |||||
 DB 17 AGGAGCGCGCTGGGCTA 1

RESULT 90
 ADA99321/c
 ID ADA99321 standard; DNA; 17 BP.
 AC ADA99321;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MD23 scanning oligonucleotide SEQ ID 310.
 XX
 KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
 KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KW developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN BP1281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 DR WPI; 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 310; 103pp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.

XX
 SQ Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 15.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 92;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 28 CTGGAGTCCTCTGAGAG 44
 |||||
 DB 17 CTGGAGCCCTTAAGAG 1

RESULT 91
 ACC67819
 ID ACC67819 standard; DNA; 17 BP.
 XX
 AC ACC67819;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5066.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLSE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 623; 738pp; French.

XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia

XX
 SQ Sequence 17 BP; 5 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 15.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 92;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 50 GAGCCAGCGAAGCTGAT 66
 |||||
 DB 1 GATCCAGAGGAGCTGAT 17

RESULT 92
 AEB61480/c
 ID AEB61480 standard; mRNA; 17 BP.
 XX
 AC AEB61480;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Human VEGF receptor 21 (Kdr) DNzyme target sequence SEQ ID 4058.
 XX
 KW VEGF receptor; angiogenesis; cancer; tumor; ocular disease;
 KW diabetic retinopathy; age related macular degeneration;
 KW angiogenesis disorder; rheumatoid arthritis; psoriasis; wound healing;
 KW endometriosis; endometroid carcinoma; gynecological bleeding disorder;
 KW menstruation disorder; premenstrual syndrome; menopause; Gynecological;
 KW Cystostatic; Ophthalmological; Antidiabetic; antiangiogenic;
 KW Antiproliferative; Antirheumatic; Antiarthritic; Vulnerary; Hemostatic;
 KW Contraceptive; ss; enzymatic nucleic acid.
 XX
 OS Homo sapiens.
 XX
 PN WO200296927-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 29-MAY-2002; 2002WO-US017674.
 XX
 PR 29-MAY-2001; 2001US-00870161.
 PR 30-NOV-2001; 2001US-0334461P.
 PR 03-MAY-2002; 2002US-00138674.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Escobedo J, Mcawiggen J, Pavco P, Stinchcomb D, Sandberg J;
 PI Gordon G;
 PI WPI; 2003-140439/13.
 DR
 XX
 PT Novel enzymatic nucleic acids, ribozymes, which modulate expression of
 PT genes encoding vascular endothelial growth factor and/or VEGF receptor,
 PT useful for inhibiting tumor angiogenesis in cell, and for treating
 PT cancer.
 XX
 PS Disclosure; SEQ ID NO 4058; 172pp; English.
 XX
 CC The invention relates to enzymatic nucleic acids (I) i.e.
 CC ribozymes/DNAzymes/Zinzymes that target and modulate expression of, genes
 CC encoding vascular endothelial growth factor (VEGF) and/or VEGF receptor
 CC (VEGFR1 and 2 encode by the Flt-1 and Kdr genes respectively). Also
 CC included are a composition comprising (I) and a carrier, administering
 CC (I) to a cell (by contacting the cell with the compound under conditions
 CC suitable for the administration), administering (I) to a cell (in
 CC conjunction with one or more other drug by contacting the cell with the
 CC compound and the other drug under conditions suitable for the
 CC administration), administering (I) to a mammal (by contacting the mammal
 CC with the compound under conditions suitable for the administration),
 CC treating (M1) a subject having endometriosis (by contacting a subject
 CC with, or administering to subject, a nucleic acid molecule (II) that
 CC modulates expression of VEGF, VEGFR1, and/or VEGFR2), a mammalian cell
 CC (III) comprising (I) and administering to a mammal (I) (in conjunction
 CC with a chemotherapeutic agent comprising contacting the mammal with the
 CC compound and the chemotherapeutic agent under conditions suitable for the
 CC administration). (I) is administered to a mammalian cell, preferably
 CC human cell in the presence of a delivery reagent which is a lipid such as
 CC cationic lipid or phospholipid, or a liposome. The enzymatic nucleic acid
 CC molecule has an endonuclease activity to cleave RNA encoded by an VEGFR1
 CC and/or VEGFR2 gene, and is in a hammerhead, inozyme, DNzyme, G-cleaver,
 CC or Ambzyme configuration. The enzymatic nucleic acids are useful for
 CC inhibiting ocular angiogenesis associated with diabetic retinopathy or
 CC age-related diabetic retinopathy, in a subject. They are also useful for
 CC inhibiting angiogenesis, preferably tumor angiogenesis in cell, and for
 CC treating a subject having a condition associated with an increased level

CC of VEGF receptor, where the condition is cancer, e.g. breast cancer, lung
 CC cancer (such as non-small cell lung carcinoma), colorectal cancer, renal
 CC cancer (such as renal cell carcinoma), pancreatic cancer. The enzymatic
 CC nucleic acids are useful for treating a subject (preferably human) having
 CC endometriosis, psoriasis, age-related macular degeneration, proliferative
 CC diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis,
 CC wound healing, endometrial carcinoma, gynecologic bleeding disorders,
 CC irregular menstrual cycles, ovulation, premenstrual syndrome, and
 CC menopausal dysfunction. the enzymatic nucleic acids are useful for birth
 CC control by inhibiting ovulation or embryonic uterine implantation. The
 CC present sequence is a target sequence from the human VEGFR2/Kdr mRNA.
 XX
 SQ Sequence 17 BP; 7 A; 4 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 15.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 92;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 60 AGCTGATGTCCTGTCAA 76
 DB 17 AGTTGCTGCTGTCAA 1
 RESULT 93
 ADX84037
 ID ADX84037 standard; DNA; 17 BP.
 XX
 AC ADX84037;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE DNA detection extension primer #36.
 XX
 KW Analysis; mass spectroscopy; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO2005014850-A2.
 XX
 PD 17-FEB-2005.
 XX
 PF 06-AUG-2004; 2004WO-US025526.
 XX
 PR 06-AUG-2003; 2003US-0493238P.
 PR 07-MAY-2004; 2004US-0568958P.
 XX
 PA (UYMA-) UNIV MASSACHUSETTS.
 PA Ginns EI, Galdzicka M;
 XX
 WPI; 2005-195764/20.
 XX
 CC Clinical assay system for assaying sample, has central controller, sample
 CC transfer module, nucleic acid extraction and measurement module,
 CC thermocycling module, primer extension module, mass spectrometry module
 CC analyzing sample.
 XX
 CC Claim 6; SEQ ID NO 108; 207pp; English.
 XX
 CC The invention relates to a system for performing an assay on a biological
 CC sample, comprising a central controller programmed to exchange
 CC information about the biological sample with an outside system or
 CC database and exchange information about the biological sample with one or
 CC more modules of the system, a sample transfer module for transferring a
 CC portion of the sample to a first container, a nucleic acid extraction
 CC module for extracting nucleic acids from cells within the portion and for
 CC transferring the portion from the first container to a second container,
 CC a nucleic acid measurement module for measuring the concentration of
 CC nucleic acids in the portion, a PCR preparation module for adding PCR
 CC reaction materials to the portion, a thermocycling module for amplifying
 CC a target sequence and extending a primer in the portion, a primer
 CC extension preparation module for adding primer extension reaction
 CC materials to the portion, a mass spectrometry preparation module for

CC removing a sample of the portion from the second container to a support
 CC for analysis by mass spectrometry and a mass spectrometry module for
 CC analyzing the sample. The invention also relates to an automated method
 CC for detecting mutations in a target gene. The diagnostic assay is an
 CC assay for detecting a pathogen in the sample. The pathogen is a virus,
 CC bacterium or fungus. The virus is a virus of the family Herpesviridae,
 CC preferably Cytomegalovirus (CMV). The system enables high accurate assays
 CC on nucleic acid sequences (e.g. clinically relevant nucleic acid
 CC sequences) using mass spectrometry. This sequence represents a DNA
 CC detection extension primer used in the scope of the invention.

XX SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 15.8%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 92;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 25 ACTCTGGAGTCTCTGA 41

Db 1 ACACAGGCGTCTCTGA 17

RESULT 94

ADM56305/c
 ID ADM56305 standard; DNA; 12 BP.

XX AC ADM56305;

XX DT 03-JUN-2004 (first entry)

XX DE Mouse SLC26A6 anion transporter protein gene splice site #24.

XX SLC26A6; SLC26A1; SLC26A2; anion transporter protein; cancer;

KW splice site; ds; mouse; murine.

XX OS Mus musculus.

XX PN WO2003072759-A2.

XX PD 04-SEP-2003.

XX PF 28-FEB-2003; 2003WO-US006469.

XX PR 28-FEB-2002; 2002US-0360275P.

XX (UYVA-) UNIV VANDERBILT.

PA (UYCA-) UNIV CASE WESTERN RESERVE.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL.

XX Mount DB, Romero MF;

XX WPI; 2003-712726/67.

XX New SLC26A6, SLC26A1 or SLC26A2 polypeptide, useful for preparing a
 PT composition for treating e.g., cancer.

XX Example 2; SEQ ID NO 37; 204pp; English.

XX The invention comprises the amino acid and coding sequences of SLC26A6,
 CC SLC26A1 and SLC26A2 anion transporter proteins. The DNA and protein
 CC sequences of the invention are useful for treating cancer. The present
 CC DNA sequence represents a splice site from the gene encoding the mouse
 CC SLC26A6 anion transporter protein.

XX SQ Sequence 12 BP; 1 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GACGGCCTGGGG 19

Db 12 GACGGCCTGGGG 1

RESULT 95

ADR70044

XX ADR70044 standard; DNA; 16 BP.

XX AC ADR70044;

XX DT 04-NOV-2004 (first entry)

XX DE Human survivin gene modulatory oligonucleotide #112.

XX ss; antiangiogenic; cytostatic; antiarteriosclerotic; antipsoriatic;
 KW antidiabetic; ophthalmological; antiarthritic; antirheumatic;
 KW antiaesthetic; antiallergic; antiinflammatory; dermatological; anti-HIV;
 KW virucide; survivin antagonist; apoptosis inhibitor;
 KW cellular proliferation inhibitor; survivin; gene expression;
 KW abnormal angiogenesis; chemotherapeutic agent; busulfan; myleran;
 KW carboplatin; paraplatin; Taxol; doxorubicin; adriamycin; atherosclerosis;
 KW psoriasis; diabetic retinopathy; rheumatoid arthritis; asthma; warts;
 KW allergic dermatitis; cancer; tumour; sarcoma; glioma; carcinoma;
 KW melanoma; osteosarcoma; Swing's sarcoma; chondrosarcoma;
 KW malignant fibrous histiocytoma; fibrosarcoma; Kaposi's sarcoma;
 KW Paclitaxel; Docetaxel.

XX OS Homo sapiens.

XX OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..16

FT /tag= b

FT /mod_base= OTHER

FT /note= "OTHER = phosphorothioate internucleotide
 linkages, all locked nucleic acid (LNA) residues are 5'-

FT modified_base 1..4

FT /tag= a

FT /mod_base= OTHER

FT /note= "OTHER = beta-D-oxy-locked nucleic acid but
 optionally DNA nucleotides, optionally phosphate
 internucleotide linkages"

FT modified_base 13..16

FT /tag= c

FT /mod_base= OTHER

FT /note= "OTHER = beta-D-oxy-locked nucleic acid but
 optionally DNA nucleotides, optionally phosphate
 internucleotide linkages"

PN WO2004069991-A2.

XX 19-AUG-2004.

XX 10-FEB-2004; 2004WO-DK000096.

XX 10-FEB-2003; 2003DK-00000183.

PR 18-NOV-2003; 2003DK-00001708.

XX (SANT-) SANTARIS PHARMA AS.

XX Hansen B, Thru CA, Petersen KD, Westergaard M, Wissenbach M;

XX WPI; 2004-625494/60.

XX New locked nucleic acid containing oligomeric compound capable of
 PT modulating survivin expression, useful for treating cancer such as breast
 PT carcinoma, lung carcinoma, etc.

XX Claim 1; SEQ ID NO 113; 122pp; English.

XX The invention relates to an oligomeric compound (I) capable of modulating
 CC survivin expression, having 8-50 nucleotides and/or nucleotide analogues,
 CC where the compound comprises a subsequence of at least 8 nucleotides or
 CC nucleotide analogues, where the subsequence is located within a sequence

CC chosen from one of 143 sequences given in the specification. (I) is
 CC useful for treating a mammal suffering from or susceptible from a disease
 CC caused by abnormal angiogenesis, by administering (I) containing one or
 CC more LNA units that are targeted to survivin. (I) is useful as a
 CC medicament and for the manufacture of a medicament for the treatment of
 CC cancer, in combination with chemotherapeutic agent such as busulfan
 CC (myleran), carboplatin (paraplatin), Taxol, doxorubicin (adriamycin),
 CC etc. (I) or a conjugate (II) containing (I) is useful in the preparation
 CC of a medicament for the treatment of atherosclerosis, psoriasis, diabetic
 CC retinopathy, rheumatoid arthritis, asthma, warts and allergic dermatitis.
 CC (I), (II) or a pharmaceutical (III) containing (I) is useful for treating
 CC cancer in the form of a solid tumour, sarcoma, glioma or carcinoma chosen
 CC from malignant melanoma, basal cell carcinoma, ovarian carcinoma, breast
 CC carcinoma, non-small cell lung cancer, renal cell carcinoma, bladder
 CC carcinoma, recurrent superficial bladder cancer, stomach carcinoma,
 CC prostatic carcinoma, pancreatic carcinoma, lung carcinoma, cervical
 CC carcinoma, cervical dysplasia, laryngeal papillomatosis, colon carcinoma,
 CC colorectal carcinoma and carcinoma tumours. The malignant melanoma is
 CC chosen from superficial spreading melanoma, nodular melanoma, lentigo
 CC maligna melanoma, acral melanoma, amelanotic melanoma, and desmoplastic
 CC melanoma. The sarcoma is chosen from osteosarcoma, Ewing's sarcoma,
 CC chondrosarcoma, malignant fibrous histiocytoma, fibrosarcoma and Kaposi's
 CC sarcoma. The treatment further involves administration of a
 CC chemotherapeutic agent such as taxanes, preferably Taxol, Paclitaxel or
 CC Docetaxel. (I), (II) or (III) is also useful for preventing or limiting
 CC apoptosis or for preventing cellular proliferation. This sequence
 CC corresponds to an antisense oligonucleotide targeted to the human
 CC survivin gene.

XX Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 CCAGCGAAGCTG 64

Db 4 CCAGCGAAGCTG 15

RESULT 96

ADW10034

ID ADW10034 standard; DNA; 16 BP.

AC ADW10034;

DT 07-APR-2005 (first entry)

XX Human survivin antisense oligonucleotide 113A, SEQ ID NO:592.

XX Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
 KW basal cell carcinoma; ovary tumor; breast tumor;
 KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
 KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
 KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
 KW sarcoma; osteosarcoma; Kaposi sarcoma; anti-HIV; glioma; cytotoxic;
 KW endocrine disease; gynecology and obstetrics; genitourinary disease;
 KW respiratory disease; musculoskeletal disease; dermatological disease;
 KW proliferative disorder; atherosclerosis; antiarteriosclerotic;
 KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
 KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
 KW cardiovascular disease; ocular disease; rheumatoid arthritis;
 KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;
 KW skin allergy; antiallergic; antiinflammatory; dermatological;
 KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
 KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;
 KW antisense oligonucleotide; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT misc_binding 1..16

FT /*tag= b

FT /bound moiety= "Bases 1568-1553 of human survivin cDNA
 FT (SEQ ID NO:1)"
 FT modified_base 1..16
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate linkages"
 FT modified_base 1..4
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D
 FT -oxy-LNA cytosines are 5-methylcytosine"
 FT modified_base 13..16
 FT /*tag= d
 FT /mod_base= OTHER
 FT /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are
 FT 5-methylcytosine"

US2005014712-A1.

20-JAN-2005.

10-FEB-2004; 2004US-00776934.

10-FEB-2003; 2003US-0446372P.

19-NOV-2003; 2003US-0523591P.

(HANS/) HANSEN B.

(THRU/) THRU C A.

(WEST/) WESTERGAARD M.

(PETE/) PETERSEN K D.

(WISS/) WISSENBACH M.

Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;

WPI; 2005-100663/11.

XX New oligomeric compound for the modulation of survivin, useful for
 XX treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
 XX rheumatoid arthritis, asthma, warts, or allergic dermatitis.

PS Example 10; SEQ ID NO 592; 264pp; English.

XX The invention relates to antisense oligonucleotides consisting of 8-50
 CC nucleotides and/or nucleotide analogs which inhibit expression of human
 CC survivin, an inhibitor of apoptosis which is also essential for cell
 CC division and angiogenesis. The antisense oligonucleotides comprise a
 CC subsequence of 8 or more nucleotides or nucleotide analogs wherein the
 CC subsequence is located within a sequence selected from ADW09444-ADW09586.
 CC The oligonucleotides preferably contain one or more (preferably 6-10)
 CC nucleotide analogs, especially a locked nucleic acid (LNA), and also
 CC preferably contain a linkage group selected from a phosphate group, a
 CC phosphorothioate group or a boranophosphate group. The invention also
 CC relates to a conjugate comprising a survivin antisense oligonucleotide of
 CC the invention and one or more non-nucleotide or non-polynucleotide
 CC moieties covalently attached to the oligonucleotide; and a pharmaceutical
 CC composition comprising a survivin antisense oligonucleotide or conjugate
 CC of the invention, optionally further comprising a chemotherapeutic agent.
 CC The survivin antisense oligonucleotides, and conjugates and compositions
 CC containing them, are useful in the treatment of cancers such as
 CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
 CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
 CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer, lung
 CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
 CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
 CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma
 CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
 CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
 CC gliomas. The survivin antisense oligonucleotides are also useful in the
 CC treatment of conditions such as atherosclerosis, psoriasis, diabetic
 CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic
 CC dermatitis. They may additionally be used for inhibiting cellular
 CC proliferation, for modulating apoptosis and for treating a disease
 CC related to abnormal angiogenesis. The survivin antisense oligonucleotides

CC of the invention are shorter than prior art survivin antisense
 CC oligonucleotides (16-mers compared to 20-25-mers), therefore having
 CC increased specificity and affinity for survivin mRNA, and also have
 CC higher biostability and cell permeability. The present sequence
 CC represents an antisense oligonucleotide targeted to the human survivin
 CC cDNA target sequence shown in ADW09443 used in an example of the
 CC invention.

XX
 SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 15.6%; Score 12; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 53 CCACGCGAAGCTG 64
 |||||
 Db 4 CCACGCGAAGCTG 15

RESULT 97
 ADW09555
 ID ADW09555 standard; DNA; 16 BP.
 AC ADW09555;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE Human survivin antisense oligonucleotide, SEQ ID NO:113.
 XX
 KW Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
 KW basal cell carcinoma; ovary tumor; breast tumor;
 KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
 KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
 KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
 KW sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;
 KW endocrine disease; gynecology and obstetrics; genitourinary disease;
 KW respiratory disease; musculoskeletal disease; dermatological disease;
 KW proliferative disorder; atherosclerosis; antiarteriosclerotic;
 KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
 KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
 KW cardiovascular disease; ocular disease; rheumatoid arthritis;
 KW arthritis; anti-rheumatic; inflammation; asthma; antiasthmatic;
 KW skin allergy; anti-allergic; anti-inflammatory; dermatological;
 KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
 KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;
 KW antisense oligonucleotide; ss.

XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_binding 1..16
 FT /tag= c
 FT /bound_moiety= "Bases 1568-1553 of human survivin cDNA
 FT (SEQ ID NO:1)"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Optionally phosphorothioate linkages when
 FT nucleotides 1-4 are beta-D-oxy-LNA. When nucleotides 1-4
 FT are unmodified, the internucleotide linkages are
 FT phosphorothioate"
 FT modified_base 1..4
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Optionally beta-D-oxy-LNAs (locked nucleic acid).
 FT All beta-D-oxy-LNA cytosines are 5-methylcytosine"
 FT modified_base 5..13
 FT /tag= d
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate linkages"
 FT modified_base 13..15
 FT /tag= e
 FT /mod_base= OTHER

FT /note= "Optionally beta-D-oxy-LNAs. All beta-D-oxy-LNA
 FT cytosines are 5-methylcytosine. Optionally
 FT phosphorothioate linkages when bases 13-15 are beta-D-oxy
 FT -LNAs. When nucleotides 13-15 are unmodified, the
 FT internucleotide linkages are phosphorothioate"
 FT modified_base 15..16
 FT /tag= f
 FT /mod_base= OTHER
 FT /note= "Optionally phosphorothioate linkage when
 FT nucleotide 16 is beta-D-oxy-LNA. This linkage is
 FT phosphorothioate when nucleotide 16 is unmodified"
 FT modified_base 16
 FT /tag= g
 FT /mod_base= OTHER
 FT /note= "Optionally beta-D-oxy-LNA. When this nucleotide
 FT is unmodified, the linkage between nucleotides 15 and 16
 FT is phosphorothioate"
 XX
 PN US2005014712-A1.
 XX
 XX 20-JAN-2005.
 XX
 XX 10-FEB-2004; 2004US-00776934.
 XX
 XX 10-FEB-2003; 2003US-0446372P.
 PR 19-NOV-2003; 2003US-0523591P.
 PR
 XX
 XX (HANS// HANSEN B.
 PA (THRU// THRU C A.
 PA (WEST// WESTERGAARD M.
 PA (PETE// PETERSEN K D.
 PA (WISS// WISSENBACH M.
 XX
 XX Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;
 XX WPI; 2005-100663/11.
 DR
 XX New oligomeric compound for the modulation of survivin, useful for
 XX treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
 FT rheumatoid arthritis, asthma, warts, or allergic dermatitis.
 FT
 XX Claim 1; SEQ ID NO 113; 264pp; English.
 PS
 XX The invention relates to antisense oligonucleotides consisting of 8-50
 XX nucleotides and/or nucleotide analogs which inhibit expression of human
 CC survivin, an inhibitor of apoptosis which is also essential for cell
 CC division and angiogenesis. The antisense oligonucleotides comprise a
 CC subsequence of 8 or more nucleotides or nucleotide analogs wherein the
 CC subsequence is located within a sequence selected from ADW09444-ADW09586.
 CC The oligonucleotides preferably contain one or more (preferably 6-10)
 CC nucleotide analogs, especially a locked nucleic acid (LNA), and also
 CC preferably contain a linkage group selected from a phosphate group, a
 CC phosphorothioate group or a boranophosphate group. The invention also
 CC relates to a conjugate comprising a survivin antisense oligonucleotide of
 CC the invention and one or more non-nucleotide or non-poly-nucleotide
 CC moieties covalently attached to the oligonucleotide; and a pharmaceutical
 CC composition comprising a survivin antisense oligonucleotide or conjugate
 CC of the invention, optionally further comprising a chemotherapeutic agent.
 CC The survivin antisense oligonucleotides, and conjugates and compositions
 CC containing them, are useful in the treatment of cancers such as
 CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
 CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
 CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
 CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
 CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma
 CC tumors); sarcomas (e.g., osteosarcoma, Kaposi's sarcoma, chondrosarcoma,
 CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
 CC gliomas. The survivin antisense oligonucleotides are also useful in the
 CC treatment of conditions such as atherosclerosis, psoriasis, diabetic
 CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic
 CC dermatitis. They may additionally be used for inhibiting cellular
 CC proliferation, for modulating apoptosis and for treating a disease

CC related to abnormal angiogenesis. The survivin antisense oligonucleotides
 CC of the invention are shorter than prior art survivin antisense
 CC oligonucleotides (16-mers compared to 20-25-mers), therefore having
 CC increased specificity and affinity for survivin mRNA, and also have
 CC higher biostability and cell permeability. The present sequence
 CC represents a specifically claimed antisense oligonucleotide targeted to
 CC the human survivin cDNA target sequence shown in ADM09443.
 XX
 SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 15.6%; Score 12; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 53 CCAGCGAAGCTG 64
 Db 4 CCAGCGAAGCTG 15
 RESULT 98
 ADM10035
 ID ADM10035 standard; DNA; 16 BP.
 XX
 AC ADM10035;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE Human survivin antisense oligonucleotide 113B, SEQ ID NO:593.
 XX
 KW Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
 KW basal cell carcinoma; ovary tumor; breast tumor;
 KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
 KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
 KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
 KW sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;
 KW endocrine disease; gynecology and obstetrics; genitourinary disease;
 KW respiratory disease; musculoskeletal disease; dermatological disease;
 KW proliferative disorder; atherosclerosis; antiarteriosclerotic;
 KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
 KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
 KW cardiovascular disease; ocular disease; rheumatoid arthritis;
 KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;
 KW skin allergy; anti-allergic; anti-inflammatory; dermatological;
 KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
 KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;
 KW antisense oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT misc_binding 1..16
 FT /tag= b
 FT /bound moiety= "Bases 1568-1553 of human survivin cDNA
 FT (SEQ ID NO:1)"
 FT modified_base 1..16
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate linkages"
 FT modified_base 1..4
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D
 FT -oxy-LNA cytosines are 5-methylcytosine"
 FT modified_base 13..15
 FT /tag= d
 FT /mod_base= OTHER
 FT /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are
 FT 5-methylcytosine"
 XX
 FN US2005014712-A1.
 XX
 PD 20-JAN-2005.
 XX

PF 10-FEB-2004; 2004US-00776934.
 XX
 PR 10-FEB-2003; 2003US-0446372P.
 PR 19-NOV-2003; 2003US-0523591P.
 XX
 PA (HANS/) HANSEN B.
 PA (THRU/) THRU C A.
 PA (WEST/) WESTERGAARD M.
 PA (PETE/) PETERSEN K D.
 PA (WISS/) WISENBACH M.
 XX
 PI Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;
 XX WPI; 2005-100663/11.
 DR
 XX
 PT New oligomeric compound for the modulation of survivin, useful for
 PT treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
 PT rheumatoid arthritis, asthma, warts, or allergic dermatitis.
 XX
 PS Example 10; SEQ ID NO 593; 264pp; English.
 XX
 CC The invention relates to antisense oligonucleotides consisting of 8-50
 CC nucleotides and/or nucleotide analogs which inhibit expression of human
 CC survivin, an inhibitor of apoptosis which is also essential for cell
 CC division and angiogenesis. The antisense oligonucleotides comprise a
 CC subsequence of 8 or more nucleotides or nucleotide analogs, wherein the
 CC subsequence is located within a sequence selected from ADM09444-ADM09586.
 CC The oligonucleotides preferably contain one or more (preferably 6-10)
 CC nucleotide analogs, especially a locked nucleic acid (LNA), and also
 CC preferably contain a linkage group selected from a phosphate group, a
 CC phosphorothioate group or a boranophosphate group. The invention also
 CC relates to a conjugate comprising a survivin antisense oligonucleotide of
 CC the invention and one or more non-nucleotide or non-polynucleotide
 CC moieties covalently attached to the oligonucleotide, and a pharmaceutical
 CC composition comprising a survivin antisense oligonucleotide or conjugate
 CC of the invention, optionally further comprising a chemotherapeutic agent.
 CC The survivin antisense oligonucleotides, and conjugates and compositions
 CC containing them, are useful in the treatment of cancers such as
 CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
 CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
 CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
 CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
 CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
 CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoid
 CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
 CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
 CC treatment of conditions such as atherosclerosis, psoriasis, diabetic
 CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic
 CC dermatitis. They may additionally be used for inhibiting cellular
 CC proliferation, for modulating apoptosis and for treating a disease
 CC related to abnormal angiogenesis. The survivin antisense oligonucleotides
 CC of the invention are shorter than prior art survivin antisense
 CC oligonucleotides (16-mers compared to 20-25-mers), therefore having
 CC increased specificity and affinity for survivin mRNA, and also have
 CC higher biostability and cell permeability. The present sequence
 CC represents an antisense oligonucleotide targeted to the human survivin
 CC cDNA target sequence shown in ADM09443 used in an example of the
 CC invention.
 XX
 SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 15.6%; Score 12; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 53 CCAGCGAAGCTG 64
 Db 4 CCAGCGAAGCTG 15
 RESULT 99
 ADM10037

ID ADW10037 standard; DNA; 16 BP.
AC ADW10037;
XX 07-APR-2005 (first entry)
XX Human survivin antisense oligonucleotide 113D, SEQ ID NO:595.
XX Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
KW basal cell carcinoma; ovary tumor; breast tumor;
KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
KW sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;
KW endocrine disease; gynecology and obstetrics; genitourinary disease;
KW respiratory disease; musculoskeletal disease; dermatological disease;
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
KW cardiovascular disease; ocular disease; rheumatoid arthritis;
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;
KW skin allergy; anti-allergic; anti-inflammatory; dermatological;
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
KW angiogenesis disorder; survivin; phosphorothioate;
KW antisense oligonucleotide; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX misc_binding 1..16 /*tag= a
FT /bound_molety= "Bases 1568-1553 of human survivin cDNA
FT (SEQ ID NO:1)"
FT modified_base 1..16
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages"
XX US2005014712-A1.
XX 20-JAN-2005.
XX 10-FEB-2004; 2004US-00776934.
XX 10-FEB-2003; 2003US-0446372P.
XX 19-NOV-2003; 2003US-0523591P.
XX (HANS/) HANSEN B.
XX (THRU/) THRU C A.
XX (WEST/) WESTERGAARD M.
XX (PETE/) PETERSEN K D.
XX (WISS/) WISSENBACH M.
XX Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;
XX WPI; 2005-100663/11.
XX New oligomeric compound for the modulation of survivin, useful for
XX treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
XX rheumatoid arthritis, asthma, warts, or allergic dermatitis.
XX Example 10; SEQ ID NO 595; 264pp; English.
XX The invention relates to antisense oligonucleotides consisting of 8-50
XX nucleotides and/or nucleotide analogs which inhibit expression of human
XX survivin, an inhibitor of apoptosis which is also essential for cell
XX division and angiogenesis. The antisense oligonucleotides comprise a
XX subsequence of 8 or more nucleotides or nucleotide analogs, wherein the
XX subsequence is located within a sequence selected from ADW09444-ADW09586.
XX The oligonucleotides preferably contain one or more (preferably 6-10)
XX nucleotide analogs, especially a locked nucleic acid (LNA), and also
XX preferably contain a linkage group selected from a phosphate group, a
XX phosphorothioate group or a boranophosphate group. The invention also

CC relates to a conjugate comprising a survivin antisense oligonucleotide of
CC the invention and one or more non-nucleotide or non-polynucleotide
CC moieties covalently attached to the oligonucleotide; and a pharmaceutical
CC composition comprising a survivin antisense oligonucleotide or conjugate
CC of the invention, optionally further comprising a chemotherapeutic agent.
CC The survivin antisense oligonucleotides, and conjugates and compositions
CC containing them, are useful in the treatment of cancers such as
CC carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma
CC tumors); sarcomas (e.g., osteosarcoma, Kaposi's sarcoma, chondrosarcoma,
CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
CC gliomas. The survivin antisense oligonucleotides are also useful in the
CC treatment of conditions such as atherosclerosis, psoriasis, diabetic
CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic
CC dermatitis. They may additionally be used for inhibiting cellular
CC proliferation, for modulating apoptosis and for treating a disease
CC related to abnormal angiogenesis. The survivin antisense oligonucleotides
CC of the invention are shorter than prior art survivin antisense
CC oligonucleotides (16-mers compared to 20-25-mers), therefore having
CC increased specificity and affinity for survivin mRNA, and also have
CC higher biostability and cell permeability. The present sequence
CC represents an antisense oligonucleotide targeted to the human survivin
CC cDNA target sequence shown in ADW09443 used in an example of the
CC invention.

SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 CCAGCGAAGCTG 64
DB |||||
4 CCAGCGAAGCTG 15

RESULT 100
ADW10036

ID ADW10036 standard; DNA; 16 BP.

XX AC ADW10036;

XX DT 07-APR-2005 (first entry)

XX DE Human survivin antisense oligonucleotide 113C, SEQ ID NO:594.

XX Antisense therapy; apoptosis stimulation; neoplasm; carcinoma; melanoma;
KW basal cell carcinoma; ovary tumor; breast tumor;
KW non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
KW stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
KW uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
KW sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;
KW endocrine disease; gynecology and obstetrics; genitourinary disease;
KW respiratory disease; musculoskeletal disease; dermatological disease;
KW proliferative disorder; atherosclerosis; antiarteriosclerotic;
KW cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
KW immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
KW cardiovascular disease; ocular disease; rheumatoid arthritis;
KW antiarthritic; antirheumatic; inflammation; asthma; antiasthmatic;
KW skin allergy; anti-allergic; anti-inflammatory; dermatological;
KW verruca vulgaris; virucide; cell proliferation; apoptosis modulation;
KW angiogenesis disorder; survivin; phosphorothioate; cytosine methylation;
KW antisense oligonucleotide; ss.

XX OS Homo sapiens.

XX PH Key Location/Qualifiers

XX FT misc_binding 1..16

XX FT /*tag= b

```

FT /bound moiety= "Bases 1568-1553 of human survivin cDNA
FT (SEQ ID NO:1)"
FT 1..4
FT /tag= a
FT /mod_base= OTHER
FT /note= "Beta-D-oxy-LNAs (locked nucleic acid). All beta-D-
FT -oxy-LNA cytosines are 5-methylcytosine"
FT 5..13
FT modified_base
FT /tag= c
FT /mod_base= OTHER
FT /note= "Phosphorothioate linkages"
FT 13..16
FT modified_base
FT /tag= d
FT /mod_base= OTHER
FT /note= "Beta-D-oxy-LNAs. All beta-D-oxy-LNA cytosines are
FT 5-methylcytosine"
XX US2005014712-A1.
XX
XX 20-JAN-2005.
XX
XX 10-FEB-2004; 2004US-00776934.
XX
XX 10-FEB-2003; 2003US-0446372P.
XX 19-NOV-2003; 2003US-0523591P.
XX
XX (HANS/) HANSEN B.
XX (THRU/) THRU C.A.
XX (WEST/) WESTERGAARD M.
XX (PETE/) PETERSEN K D.
XX (WISS/) WISSENBACH M.
XX
XX Hansen B, Thru CA, Westergaard M, Petersen KD, Wissenbach M;
XX WPI; 2005-100663/11.
XX
XX New oligomeric compound for the modulation of survivin, useful for
XX treating e.g. cancers, atherosclerosis, psoriasis, diabetic retinopathy,
XX rheumatoid arthritis, asthma, warts, or allergic dermatitis.
XX
XX Example 10; SEQ ID NO 594; 264pp; English.
XX
XX The invention relates to antisense oligonucleotides consisting of 8-50
XX nucleotides and/or nucleotide analogs which inhibit expression of human
XX survivin, an inhibitor of apoptosis which is also essential for cell
XX division and angiogenesis. The antisense oligonucleotides comprise a
XX subsequence of 8 or more nucleotides or nucleotide analogs, wherein the
XX subsequence is located within a sequence selected from ADM09444-ADM09586.
XX The oligonucleotides preferably contain one or more (preferably 6-10)
XX nucleotide analogs, especially a locked nucleic acid (LNA), and also
XX preferably contain a linkage group selected from a phosphate group, a
XX phosphorothioate group or a boranophosphate group. The invention also
XX relates to a conjugate comprising a survivin antisense oligonucleotide of
XX the invention and one or more non-nucleotide or non-polynucleotide
XX moieties covalently attached to the oligonucleotide; and a pharmaceutical
XX composition comprising a survivin antisense oligonucleotide or conjugate
XX of the invention, optionally further comprising a chemotherapeutic agent.
XX The survivin antisense oligonucleotides, and conjugates and compositions
XX containing them, are useful in the treatment of cancers such as
XX carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
XX carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
XX carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
XX stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
XX carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
XX papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma
XX tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
XX malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
XX gliomas. The survivin antisense oligonucleotides are also useful in the
XX treatment of conditions such as atherosclerosis, psoriasis, diabetic
XX retinopathy, rheumatoid arthritis, asthma, warts, and allergic
XX dermatitis. They may additionally be used for inhibiting cellular
XX proliferation, for modulating apoptosis and for treating a disease
XX related to abnormal angiogenesis. The survivin antisense oligonucleotides

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CC of the invention are shorter than prior art survivin antisense
CC oligonucleotides (16-mers compared to 20-25-mers), therefore having
CC increased specificity and affinity for survivin mRNA, and also have
CC higher biostability and cell permeability. The present sequence
CC represents an antisense oligonucleotide targeted to the human survivin
CC cDNA target sequence shown in ADM09443 used in an example of the
CC invention.
XX
XX SQ Sequence 16 BP; 3 A; 4 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 15.6%; Score 12; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 92;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 53 CCAGCGAAGCTG 64
XX Db 4 CCAGCGAAGCTG 15
XX
XX RESULT 101
XX ABN10030
XX ID ABN10030 standard; DNA; 17 BP.
XX
XX AC ABN10030;
XX
XX DT 29-MAY-2002 (first entry)
XX
XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10022.
XX
XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200192524-A2.
XX
XX PD 06-DEC-2001.
XX
XX PF 25-MAY-2001; 2001WO-US016981.
XX
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 05-FEB-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 10022; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify

```

CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCCTC 38

Db 6 TCTGGAGTCCTC 17

RESULT 102

ACN73120
 ID ACN73120 standard; DNA; 17 BP.

XX ACN73120;

DT 02-DEC-2004 (first entry)

XX Human GDMPLP-1 probe SEQ ID NO:10022.

XX Human; ss; probe; myosin-like protein-1; hGDMPLP-1;

KW hGDMPLP-1 agonist hGDMPLP antagonist; hGDMPLP inhibitor; heart disorder;
 KW skeletal muscle function.

XX Homo sapiens.

XX US2004137589-A1.

XX 15-JUL-2004.

XX 26-NOV-2003; 2003US-00723361.

XX 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 30-JAN-2001; 2001WO-US000661.

XX 30-JAN-2001; 2001WO-US000662.

XX 30-JAN-2001; 2001WO-US000663.

XX 30-JAN-2001; 2001WO-US000664.

XX 30-JAN-2001; 2001WO-US000665.

XX 30-JAN-2001; 2001WO-US000666.

XX 30-JAN-2001; 2001WO-US000667.

XX 30-JAN-2001; 2001WO-US000668.

XX 30-JAN-2001; 2001WO-US000669.

XX 30-JAN-2001; 2001WO-US000670.

XX 05-FEB-2001; 2001US-0266860P.

XX 25-MAY-2001; 2001US-00866108.

XX (GUYY/) GU Y.

XX (JIYY/) JI Y.

XX (FENN/) PENN S G.

XX (HANZ/) HANZEL D K.

PA (RANK/) RANK D.
 PA (CHEN/) CHEN W.
 PA (SHAN/) SHANNON M E.

PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank D, Chen W, Shannon ME;

XX WPI; 2004-533378/51.

XX Novel myosin-like protein-1, useful for treating or preventing disorder
 PT associated with decreased expression or activity of human genome-derived
 PT myosin-like protein-1 such as disorder of heart and/or skeletal muscle
 PT function.

XX Disclosure; SEQ ID NO 10022; Opp; English.

XX The invention relates to a novel polypeptide (I) comprising a sequence
 CC (S1) of myosin-like protein-1 (hGDMPLP-1) having 2568 amino acids fully
 CC defined in the specification, a fragment of at least 8 amino acids of
 CC (S1), 95% deviation from (S1) which are conservative substitutions, and
 CC 65% identity to (S1). A polypeptide of the invention acts as an agonist or
 CC antagonist of hGDMPLP-1, or as an inhibitor of hGDMPLP-1 activity. A
 CC pharmaceutical composition of the invention is useful for treating or
 CC preventing a disorder associated with decreased expression or activity of
 CC hGDMPLP-1, such as a disorder of heart and/or skeletal muscle function.
 CC The present sequence represents a 17-mer nucleotide, used in the
 CC invention for scanning the sequence represented in ACN63103

XX Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 15.6%; Score 12; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 TCTGGAGTCCTC 38

Db 6 TCTGGAGTCCTC 17

RESULT 103

AAH18889

ID AAH18889 standard; DNA; 15 BP.

XX AAH18889;

XX 21-JUN-2001 (first entry)

XX UCP3 polymorphism detection allele specific primer #2.

XX UCP3; uncoupling protein 3; polymorphism; obesity; diabetes mellitus; ss.

XX Homo sapiens.

XX WO200118232-A2.

XX 15-MAR-2001.

XX 08-SEP-2000; 2000WO-US024784.

XX 08-SEP-1999; 99US-0152789P.

XX (GENA-) GENAISANCE PHARM INC.

XX (STEP/) STEPHENS J C.

XX Chew A, Choi JY, Denton RR, Nandabalan K;

XX WPI; 2001-218562/22.

XX Nucleic acids encoding uncoupling protein 3 (mitochondrial, proton
 PT carrier) (UCP3) proteins comprising single nucleotide polymorphisms,
 PT useful for the design of drugs for treating obesity.

XX Claim 15; Page 22; 94pp; English.

CC The present invention relates to the human uncoupling protein 3
 CC (mitochondrial, proton carrier) (UCP3) gene and polymorphisms. The
 CC polymorphisms are associated with obesity, especially diabetes mellitus
 CC associated obesity. They polymorphisms may be identified and analysed to
 CC determine whether an individual is susceptible to obesity and may be used
 CC as the basis for targeted design of drugs to treat obesity. The present
 CC sequence was used in the identification and amplification of UCP3
 CC polymorphisms
 XX
 SQ Sequence 15 BP; 4 A; 5 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 44 GGTAAAGAGCCAGCG 58
 DB 1 GGCACAGAGCCAGCG 15
 ||| ||||| ||||| |||||

RESULT 104
 AAF52028
 ID AAF52028 standard; DNA; 15 BP.
 XX
 AC AAF52028;
 DT 30-MAR-2001 (first entry)
 XX
 DE IGF-I oligonucleotide #2988.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 80; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, ptyriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a

CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTGATGT 68
 DB 1 CAGCGCTGCTGATGT 15
 ||||| ||||| ||||| |||||

RESULT 105
 ABL53810
 ID ABL53810 standard; DNA; 15 BP.
 XX
 AC ABL53810;
 XX
 DT 25-JUN-2002 (first entry)
 XX
 DE Equine infectious anemia virus DU gene coding sequence 3' fragment.
 XX
 KW EIAV; dUTPase; enzyme; DU gene; vaccine; infection; model; gene; ss.
 XX
 OS Equine infectious anemia virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..15
 FT /tag= a
 FT /product= "S2 peptide"
 FT /note= "the CDS does not include a start or stop codon"
 XX
 PN WO200220051-A2.
 XX
 PD 14-MAR-2002.
 XX
 PF 06-SEP-2001; 2001WO-US027604.
 XX
 PR 09-SEP-2000; 2000US-00659030.
 XX
 PA (ALKU) AKZO NOBEL NV.
 XX
 PI Montelaro RC, Puffer B, Li F, Issel C, Hennessey KJ, Brown KK;
 XX
 DR WPI; 2002-339776/37.
 DR P-PSDB; ABB75741.
 XX
 PT Infecting equine with equine infectious anemia virus in order to
 PT reproduce natural infection model which is useful for evaluating
 PT immunogenicity of EIAV vaccine, involves administering a median horse
 PT infective dose to equine.
 XX
 PS Example 1; Fig 5; 49pp; English.
 XX
 CC The present sequence is a 3' fragment of the dUTPase (DU) gene coding
 CC sequence of equine infectious anemia virus (EIAV). In the mutated
 CC EIAVdeltaDU gene of the invention, this portion of the DU gene is ligated
 CC to a 5' fragment (see ABL53809) of the gene, to produce a DU gene-deleted
 CC construct (see ABL53811). The invention describes a vaccine for
 CC effectively and safely immunising mammals, especially equids, from
 CC disease caused by EIAV, the vaccine being tested for efficacy or
 CC immunogenicity using an EIA equine challenge model of the invention. The
 CC vaccine is a gene-deleted EIAV, e.g. a DU gene-deleted EIAV, which lacks
 CC the ability to express the mutated gene protein in vivo, this lack of
 CC expression being useful to differentiate vaccinated from non-vaccinated
 CC or infected mammals. The multiple low dose EIA challenge model of the
 CC invention can be used to determine the efficacy of vaccines, treatments
 CC and diagnostic tests
 XX

SQ Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGGAT 21
 ||||| ||||| |||||
 Db 1 AGACAGCCTTGGGAT 15

RESULT 106
 AAS19731
 ID AAS19731 standard; DNA; 15 BP.
 XX AC AAS19731;
 XX AC AAS19731;
 XX DT 08-MAY-2002 (first entry)
 XX ASO probe #28 to detect human RANGAP1 gene polymorphisms.
 DE Human; single nucleotide polymorphism; SNP; RANGAP1;
 KW haplotyping chromosome 22q13.2-q13.31; Ran GTPase activating protein 1;
 KW genotyping; cancer; irregular cell cycle associated disorder; ASO; probe;
 KW ss; allele-specific oligonucleotide.
 XX Homo sapiens.
 XX WO200179240-A2.
 XX PD 25-OCT-2001.
 XX PF 17-APR-2001; 2001WO-US012455.
 XX PR 17-APR-2000; 2000US-0198072P.
 XX PA (GENA-) GENAISSANCE PHARM INC.
 XX PI Chew A, Choi JY, Koshy B;
 XX WPI; 2002-075068/10.
 XX Genotyping human Ran GTPase activating protein 1 gene of individual for
 PT determining haplotype of individual, involves determining identity of
 PT nucleotide pair at specific polymorphic sites for two copies of the gene.
 XX Claim 15; Page 14; 148pp; English.
 CC The present invention relates to novel single nucleotide polymorphisms
 CC (SNPs) in the human Ran GTPase activating protein 1 (RANGAP1) gene
 CC located on chromosome 22q13.2-q13.31, and methods for haplotyping and/or
 CC genotyping the RANGAP1 gene. The methods of the invention make use of
 CC allele-specific oligonucleotides (ASOs) as probes and primers and/or
 CC primer-extension oligonucleotides for detecting the RANGAP1 gene
 CC polymorphisms. The polynucleotides and screened compounds are useful for
 CC treatment of diseases associated with RANGAP1 activity, such as cancer
 CC and other disorders associated with an irregular cell cycle. AAS19704-
 CC AAS19742 represent ASO probes for detecting human RANGAP1 gene
 CC polymorphisms
 XX Sequence 15 BP; 2 A; 4 C; 4 G; 4 T; 0 U; 1 Other;
 Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 GAAGCTGATGCTCTG 72
 ||||| ||||| |||||
 Db 1 GAACCTGTGTCTCTG 15

RESULT 107
 ABL53795

SD Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGGAT 21
 ||||| ||||| |||||
 Db 1 AGACAGCCTTGGGAT 15

RESULT 108
 ACF57576
 ID ACF57576 standard; DNA; 15 BP.

SD Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGGAT 21
 ||||| ||||| |||||
 Db 1 AGACAGCCTTGGGAT 15

RESULT 109
 ABL53795
 ID ABL53795 standard; DNA; 15 BP.
 AC ABL53795;
 DT 25-JUN-2002 (first entry)
 XX Equine infectious anemia virus DU gene 3' fragment.
 DE EIAV; dUTPase; enzyme; DU gene; vaccine; diagnosis; gene; ss.
 XX Equine infectious anemia virus.
 XX Key Location/Qualifiers
 CDS 1..15
 FT /*tag= a
 FT /product= "S2 peptide"
 FT /partial
 FT /note= "the CDS does not include a start or stop codon"
 XX WO200220041-A2.
 XX PD 14-MAR-2002.
 XX PP 06-SEP-2001; 2001WO-US027601.
 XX PR 09-SEP-2000; 2000US-00658547.
 XX PA (ALKU) AKZO NOBEL NV.
 XX PI Montaloro RC, Puffer B, Li F, Issel C, Hennessey KJ, Brown KK;
 XX WPI; 2002-339773/37.
 XX DR P-PSDB; ABB75736.
 XX Novel vaccine comprising gene-mutated equine infectious anemia virus
 PT which lacks ability to express mutated gene protein in vivo, useful for
 PT immunizing horses against disease caused by equine infectious anemia
 PT virus.
 XX Example 6; Fig 5; 54pp; English.
 CC The present sequence is a 3' fragment of the dUTPase (DU) gene coding
 CC sequence of equine infectious anemia virus (EIAV). In the mutated
 CC EIAVdeltaDU gene of the invention, this portion of the DU gene is ligated
 CC to a 5' fragment (see ABL53794) of the gene, to generate the sequence
 CC given in ABL53796. Two StyI sites flanking the gene are used to create
 CC the deletion, removing 80% of the DU coding sequence, including 4 of 5
 CC conserved amino acid motifs. The invention relates to EIA vaccines that
 CC provide immunity to mammals, especially to equines, from infection with
 CC EIAV, and which allow differentiation between vaccinated and non-
 CC vaccinated, but exposed, animals. The vaccine has at least 1 mutation in
 CC the EIAV, e.g. the present DU gene-mutated EIAV construct, which produces
 CC a non-functional gene in the vaccine virus. Deletion of the DU gene does
 CC not reduce the ability of the mutated EIAV to replicate in cell culture,
 CC allowing large-scale vaccine production. The vaccine cannot cause
 CC clinical disease or spread to other animals. The mutated region can also
 CC be used as an insertion point for foreign genes, using EIAV as a vector
 CC for vaccination against diseases other than EIA
 XX Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 AGACGGCTGGGAT 21
 ||||| ||||| |||||
 Db 1 AGACAGCCTTGGGAT 15

RESULT 108
 ACF57576
 ID ACF57576 standard; DNA; 15 BP.

```

XX ACFS57576;
XX
XX 22-APR-2004 (first entry)
XX
XX Human ALDOB gene allele-specific primer SEQ ID NO: 27.
XX
XX Human; ALDOB; fructose-bisphosphate aldolase B; SNP;
XX single nucleotide polymorphism; primer; probe; ss.
XX
XX Homo sapiens.
XX
XX WO2003091454-A1.
XX
XX 06-NOV-2003.
XX
XX 26-APR-2002; 2002WO-US013328.
XX
XX 26-APR-2002; 2002WO-US013328.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Kazemi A, Koshy B;
XX
XX WPI; 2003-877338/81.
XX
XX Claim 39; Page 14; Opp; English.
XX
XX The present invention provides the protein and coding sequences of human
XX fructose-bisphosphate aldolase B (ALDOB) and single nucleotide
XX polymorphisms (SNPs) which have been identified in each sequence. The
XX method of haplotyping the sequences is useful for haplotyping the
XX fructose-bisphosphate aldolase B (ALDOB) gene of an individual or for
XX validating the ALDOB protein as a candidate target for treating a medical
XX condition predicted to be associated with ALDOB activity. The present
XX sequence is an allele-specific primer/probe used to identify the
XX haplotype of the human ALDOB gene in the exemplification of the invention
XX
XX Sequence 15 BP; 6 A; 2 C; 5 G; 1 T; 0 U; 1 Other;
XX
XX Query Match 15.3%; Score 11.8; DB 1; Length 15;
XX Best Local Similarity 86.7%; Pred. No. 92;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGAGCCA 55
DB 1 AGAGGTCAAGAGCRA 15
||||| ||||| |||||

RESULT 109
ADJ82347
ID ADJ82347 standard; DNA; 15 BP.
XX
XX ADJ82347;
XX
XX 06-MAY-2004 (first entry)
XX
XX KLM5Y-encoding nucleotide #75.
XX
XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
XX myeloproliferative disease; blood vessel proliferative disease;
XX angiogenesis.
XX
XX Synthetic.
XX
XX WO2003045973-A2.
XX
XX 05-JUN-2003.
XX
XX 30-SEP-2002; 2002WO-US031165.
XX

XX 28-NOV-2001; 2001US-0333476P.
XX (BECT ) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX Dean C, Heidaran M, Spargo CA;
XX
XX WPI; 2003-505179/47.
XX
XX New peptides having growth inhibitory action, useful for inhibiting tumor
XX or cancer cell proliferation, or for treating fibrotic disorders,
XX myeloproliferative diseases, and blood vessel proliferative (angiogenic)
XX disorders.
XX
XX Disclosure; SEQ ID NO 128; 48pp; English.
XX
XX The invention relates to an isolated peptide or polypeptide (I) of no
XX more than about 50 amino acid residues which when contacted with cells in
XX which a platelet-derived growth factor receptor (PDGF-R) is activated in
XX an autocrine manner, inhibits the growth of these cells. The isolated
XX peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
XX Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
XX Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
XX proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
XX sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
XX or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
XX ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
XX muscle or bone cell. The peptides are also useful for treating fibrotic
XX disorders, myeloproliferative diseases, and blood vessel proliferative
XX (angiogenic) disorders. This sequence represents a possible nucleotide
XX encoding the P3 peptide.
XX
XX Sequence 15 BP; 4 A; 3 C; 2 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 15.3%; Score 11.8; DB 1; Length 15;
XX Best Local Similarity 86.7%; Pred. No. 92;
XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AGCTGATGTCCTGT 73
DB 1 AGCTTATGTCCTAT 15
||||| ||||| |||||

RESULT 110
ADJ82397
ID ADJ82397 standard; DNA; 15 BP.
XX
XX ADJ82397;
XX
XX 06-MAY-2004 (first entry)
XX
XX KLM5Y-encoding nucleotide #125.
XX
XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
XX myeloproliferative disease; blood vessel proliferative disease;
XX angiogenesis.
XX
XX Synthetic.
XX
XX WO2003045973-A2.
XX
XX 05-JUN-2003.
XX
XX 30-SEP-2002; 2002WO-US031165.
XX
XX 28-NOV-2001; 2001US-0333476P.
XX
XX (BECT ) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX Dean C, Heidaran M, Spargo CA;
XX

```


XX WPI; 2003-505179/47.
 XX New peptides having growth inhibitory action, useful for inhibiting tumor
 PT or cancer cell proliferation, or for treating fibrotic disorders,
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
 PT disorders.
 XX Disclosure; SEQ ID NO 178; 48pp; English.
 XX The invention relates to an isolated peptide or polypeptide (I) of no
 CC more than about 50 amino acid residues which when contacted with cells in
 CC which a platelet-derived growth factor receptor (PDGFR) is activated in
 CC an autocrine manner, inhibits the growth of these cells. The isolated
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
 CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
 CC muscle or bone cell. The peptides are also useful for treating fibrotic
 CC disorders, myeloproliferative diseases, and blood vessel proliferative
 CC (angiogenic) disorders. This sequence represents a possible nucleotide
 CC encoding the P3 peptide.
 XX Sequence 15 BP; 5 A; 2 C; 3 G; 5 T; 0 U; 0 Other;
 SQ Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 59 AAGCTGATGTCCTGT 73
 Db 1 AAGCTGATGTCATAT 15
 RESULT 111
 ADJ82379
 ID ADJ82379 standard; DNA; 15 BP.
 XX AC ADJ82379;
 XX 06-MAY-2004 (first entry)
 DE KLMYS-encoding nucleotide #107.
 XX SS; cytostatic; platelet-derived growth factor receptor; PDGFR; cancer;
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
 KW myeloproliferative disease; blood vessel proliferative disease;
 KW angiogenesis.
 XX OS Synthetic.
 XX WO2003045973-A2.
 XX 05-JUN-2003.
 XX 30-SEP-2002; 2002WO-US031165.
 XX 28-NOV-2001; 2001US-0333476P.
 XX (BECT) BECTON DICKINSON & CO.
 XX (HAAL/) HAALAND P D.
 XX Dean C, Heidaran M, Spargo CA;
 XX WPI; 2003-505179/47.
 XX New peptides having growth inhibitory action, useful for inhibiting tumor
 PT or cancer cell proliferation, or for treating fibrotic disorders,
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)

PT disorders.
 XX Disclosure; SEQ ID NO 160; 48pp; English.
 XX The invention relates to an isolated peptide or polypeptide (I) of no
 CC more than about 50 amino acid residues which when contacted with cells in
 CC which a platelet-derived growth factor receptor (PDGFR) is activated in
 CC an autocrine manner, inhibits the growth of these cells. The isolated
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
 CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
 CC muscle or bone cell. The peptides are also useful for treating fibrotic
 CC disorders, myeloproliferative diseases, and blood vessel proliferative
 CC (angiogenic) disorders. This sequence represents a possible nucleotide
 CC encoding the P3 peptide.
 XX Sequence 15 BP; 5 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
 SQ Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 59 AAGCTGATGTCCTGT 73
 Db 1 AAGCTGATGTCCTAT 15
 RESULT 112
 ADJ82331
 ID ADJ82331 standard; DNA; 15 BP.
 XX AC ADJ82331;
 XX 06-MAY-2004 (first entry)
 DE KLMYS-encoding nucleotide #59.
 XX SS; cytostatic; platelet-derived growth factor receptor; PDGFR; cancer;
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
 KW myeloproliferative disease; blood vessel proliferative disease;
 KW angiogenesis.
 XX OS Synthetic.
 XX WO2003045973-A2.
 XX 05-JUN-2003.
 XX 30-SEP-2002; 2002WO-US031165.
 XX 28-NOV-2001; 2001US-0333476P.
 XX (BECT) BECTON DICKINSON & CO.
 XX (HAAL/) HAALAND P D.
 XX Dean C, Heidaran M, Spargo CA;
 XX WPI; 2003-505179/47.
 XX New peptides having growth inhibitory action, useful for inhibiting tumor
 PT or cancer cell proliferation, or for treating fibrotic disorders,
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
 PT disorders.
 XX Disclosure; SEQ ID NO 112; 48pp; English.
 XX The invention relates to an isolated peptide or polypeptide (I) of no
 CC more than about 50 amino acid residues which when contacted with cells in

CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
CC an autocrine manner, inhibits the growth of these cells. The isolated
CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
CC Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-
CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (1) is useful for inhibiting cell
CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
CC muscle or bone cell. The peptides are also useful for treating fibrotic
CC disorders, myeloproliferative diseases, and blood vessel proliferative
CC (angiogenic) disorders. This sequence represents a possible nucleotide
CC encoding the P3 peptide.
XX
SQ Sequence 15 BP; 5 A; 3 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 15.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 92;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCTGT 73
Db 1 AAATGATGTCCTAT 15

RESULT 113
ADJ82363
ID ADJ82363 standard; DNA; 15 BP.
AC ADJ82363;
XX
XX 06-MAY-2004 (first entry)
DE KLMSY-encoding nucleotide #91.
XX
XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
KW myeloproliferative disease; blood vessel proliferative disease;
KW angiogenesis.
XX
XX Synthetic.
XX WO2003045973-A2.
XX
XX 05-JUN-2003.
XX
XX 30-SEP-2002; 2002WO-US031165.
XX
XX 28-NOV-2001; 2001US-0333476P.
XX
XX (BECT) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX Dean C, Heidaran M, Spargo CA;
XX WPI; 2003-505179/47.
XX
XX New peptides having growth inhibitory action, useful for inhibiting tumor
XX or cancer cell proliferation, or for treating fibrotic disorders,
XX myeloproliferative diseases, and blood vessel proliferative (angiogenic)
XX disorders.
XX
XX Disclosure; SEQ ID NO 144; 48pp; English.
XX
XX The invention relates to an isolated peptide or polypeptide (1) of no
XX more than about 50 amino acid residues which when contacted with cells in
XX which a platelet-derived growth factor receptor (PDGF-R) is activated in
XX an autocrine manner, inhibits the growth of these cells. The isolated
XX peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-
XX Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-
XX Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (1) is useful for inhibiting cell
XX proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
XX sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
XX or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
XX ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
XX muscle or bone cell. The peptides are also useful for treating fibrotic
XX disorders, myeloproliferative diseases, and blood vessel proliferative
XX (angiogenic) disorders. This sequence represents a possible nucleotide
XX encoding the P3 peptide.

CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
CC muscle or bone cell. The peptides are also useful for treating fibrotic
CC disorders, myeloproliferative diseases, and blood vessel proliferative
CC (angiogenic) disorders. This sequence represents a possible nucleotide
CC encoding the P3 peptide.
XX
SQ Sequence 15 BP; 4 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 15.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 92;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 59 AAGCTGATGTCCTGT 73
Db 1 AAGCTGATGTCCTAT 15

RESULT 114
ADJ82387
ID ADJ82387 standard; DNA; 15 BP.
XX
XX ADJ82387;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
DE KLMSY-encoding nucleotide #115.
XX
XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
KW myeloproliferative disease; blood vessel proliferative disease;
KW angiogenesis.
XX
XX Synthetic.
XX WO2003045973-A2.
XX
XX 05-JUN-2003.
XX
XX 30-SEP-2002; 2002WO-US031165.
XX
XX 28-NOV-2001; 2001US-0333476P.
XX
XX (BECT) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX Dean C, Heidaran M, Spargo CA;
XX WPI; 2003-505179/47.
XX
XX New peptides having growth inhibitory action, useful for inhibiting tumor
XX or cancer cell proliferation, or for treating fibrotic disorders,
XX myeloproliferative diseases, and blood vessel proliferative (angiogenic)
XX disorders.
XX
XX Disclosure; SEQ ID NO 168; 48pp; English.
XX
XX The invention relates to an isolated peptide or polypeptide (1) of no
XX more than about 50 amino acid residues which when contacted with cells in
XX which a platelet-derived growth factor receptor (PDGF-R) is activated in
XX an autocrine manner, inhibits the growth of these cells. The isolated
XX peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-
XX Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-
XX Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (1) is useful for inhibiting cell
XX proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
XX sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
XX or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
XX ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
XX muscle or bone cell. The peptides are also useful for treating fibrotic
XX disorders, myeloproliferative diseases, and blood vessel proliferative
XX (angiogenic) disorders. This sequence represents a possible nucleotide
XX encoding the P3 peptide.

CC encoding the P3 peptide.
 SQ Sequence 15 BP; 5 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGT 73
 DB 1 AAGCTGATGTCGTAT 15

RESULT 115
 ADJ82399
 ID ADJ82399 standard; DNA; 15 BP.
 XX
 AC ADJ82399;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE KLMYSY-encoding nucleotide #127.
 XX
 KW ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
 KW myeloproliferative disease; blood vessel proliferative disease;
 KW angiogenesis.
 XX
 OS Synthetic.
 XX
 PN W02003045973-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 30-SEP-2002; 2002WO-US031165.
 XX
 PR 28-NOV-2001; 2001US-0333476P.
 XX
 PA (BECT) BECTON DICKINSON & CO.
 PA (HAAL/) HAALAND P D.
 XX
 PI Dean C, Heidaran M, Spargo CA;
 XX
 DR WPI; 2003-505179/47.
 XX
 PT New peptides having growth inhibitory action, useful for inhibiting tumor
 PT or cancer cell proliferation, or for treating fibrotic disorders,
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
 PT disorders.
 XX
 PS Disclosure; SEQ ID NO 180; 48pp; English.
 XX
 CC The invention relates to an isolated peptide or polypeptide (I) of no
 CC more than about 50 amino acid residues which when contacted with cells in
 CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
 CC an autocrine manner, inhibits the growth of these cells. The isolated
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
 CC Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
 CC muscle or bone cell. The peptides are also useful for treating fibrotic
 CC disorders, myeloproliferative diseases, and blood vessel proliferative
 CC (angiogenic) disorders. This sequence represents a possible nucleotide
 CC encoding the P3 peptide.
 XX
 SQ Sequence 15 BP; 4 A; 2 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGT 73
 DB 1 AAGCTGATGTCGTAT 15

RESULT 116
 ADJ82393
 ID ADJ82393 standard; DNA; 15 BP.
 XX
 AC ADJ82393;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE KLMYSY-encoding nucleotide #121.
 XX
 KW ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
 KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
 KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
 KW myeloproliferative disease; blood vessel proliferative disease;
 KW angiogenesis.
 XX
 OS Synthetic.
 XX
 PN W02003045973-A2.
 XX
 PD 05-JUN-2003.
 XX
 PF 30-SEP-2002; 2002WO-US031165.
 XX
 PR 28-NOV-2001; 2001US-0333476P.
 XX
 PA (BECT) BECTON DICKINSON & CO.
 PA (HAAL/) HAALAND P D.
 XX
 PI Dean C, Heidaran M, Spargo CA;
 XX
 DR WPI; 2003-505179/47.
 XX
 PT New peptides having growth inhibitory action, useful for inhibiting tumor
 PT or cancer cell proliferation, or for treating fibrotic disorders,
 PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
 PT disorders.
 XX
 PS Disclosure; SEQ ID NO 174; 48pp; English.
 XX
 CC The invention relates to an isolated peptide or polypeptide (I) of no
 CC more than about 50 amino acid residues which when contacted with cells in
 CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
 CC an autocrine manner, inhibits the growth of these cells. The isolated
 CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
 CC Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
 CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
 CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
 CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
 CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
 CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
 CC muscle or bone cell. The peptides are also useful for treating fibrotic
 CC disorders, myeloproliferative diseases, and blood vessel proliferative
 CC (angiogenic) disorders. This sequence represents a possible nucleotide
 CC encoding the P3 peptide.
 XX
 SQ Sequence 15 BP; 4 A; 2 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 15.3%; Score 11.8; DB 1; Length 15;
 Best Local Similarity 86.7%; Pred. No. 92;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCTGT 73
 DB 1 AAGCTGATGTCGTAT 15

RESULT 117
ADT41519
XX ID ADT41519 standard; DNA; 15 BP.
XX AC
XX ADT41519;
XX DT 27-JAN-2005 (first entry)
XX DE EIAV dUTPase (DU) C-terminal DNA.
XX EIAV; S2 protein; vaccine; envelope protein; Tat protein;
KW lentiviral disease; EIAV infection; ds; dUTPase; DU.
XX OS Equine infectious anemia virus.
XX US2004219166-A1.
XX PD 04-NOV-2004.
XX PF 24-JUL-2003; 2003US-00627568.
XX PR 09-SEP-2000; 2000US-00658547.
XX PR 26-JUN-2002; 2002US-00180626.
XX (MONT/) MONTELABO R C.
PA (CRAI/) CRAIGO J.
PA (LIFF/) LI F.
XX Montelaro RC, Craigo J, Li F;
XX WPI; 2004-774916/76.
DR P-PSDB; ADT41520.
XX New construct comprising gene-mutated equine infectious anemia virus
PT (EIAV) for providing immunity from diseases caused by EIAV and allowing
PT diagnostic differentiation between vaccinated and non-vaccinated mammals
PT (i.e. horses).
XX Example 6; Fig 5; 3lpp; English.
XX The invention relates to a construct comprising a gene-mutated equine
CC infectious anemia virus (EIAV) comprising two redundant stop codons and a
CC deletion (in the S2 protein) where the virus lacks the ability to express
CC the mutated gene protein in vivo and where the lack of expression can be
CC used to differentiate vaccinated from non-vaccinated or infected mammals.
CC Also included are a diagnostic test for differentiating mammals
CC vaccinated with the above construct from non-vaccinated mammals/infected
CC mammals (comprising one or more reagents for demonstrating the absence
CC of a normal EIAV gene expression product or a normal gene sequence in
CC mammals vaccinated with the gene-mutated construct and a measurable level
CC of the expression product or amount of the normal gene sequence in
CC infected mammals) and a method of differentiating a vaccinated mammal
CC from a non-vaccinated mammal (comprising obtaining a sample from a test
CC mammal, and analysing the sample for the presence of a gene expression
CC product normally produced by wild-type EIAV but not produced by the EIAV
CC construct cited above). The two redundant stop codons are inserted into
CC the S2 open reading frame at positions corresponding to amino acids Gly5
CC and Gly18. The stop codon does not affect normal expression of the
CC envelope protein. The deletion is a deletion of about 6-25 base pairs and
CC is located at least 7 base pairs downstream of the stop codon of the
CC second coding region of Tat. The deletion does not interrupt the splice
CC donor 2 site downstream of the stop codon of the second coding region of
CC TAR and upstream of the initiation codon of the S2 open reading frame.
CC The generation of the stop codon at Gly5 further comprises the insertion
CC of a restriction endonuclease site where the restriction endonuclease is
CC a molecular marker for differentiating between wild type EIAV and the
CC gene-mutated EIAV. The construct is useful for immunising mammals (e.g.
CC horses) against lentiviral diseases, particularly EIAV infection. The
CC construct and method may also be used for differentiating vaccinated
CC mammals from non-vaccinated or infected mammals. Deletions were also
CC contemplated in the DU (dUTPase) gene of EIAV. The present sequence is
CC the wild-type EIAV DU 5' or 3' end.

XX SQ Sequence 15 BP; 4 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 15.3%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 92;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 7 AGACGGCCTGGGAT 21
DB 1 AGACGGCCTGGGAT 15
RESULT 118
AAQ32194/c
XX ID AAQ32194 standard; DNA; 16 BP.
XX AC AAQ32194;
XX DT 25-MAR-2003 (revised)
DT 27-APR-1993 (first entry)
XX DE Consensus 16n repeat of major IE gene promoter region.
XX Human; cytomegalovirus; CMV; immediate-early; transcription; ss.
XX Synthetic.
XX US5168062-A.
XX PD 01-DEC-1992.
XX PF 10-SEP-1990; 90US-00582130.
XX PR 30-JAN-1985; 85US-00696617.
PR 22-MAY-1987; 87US-00058662.
PR 05-OCT-1988; 88US-00256134.
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX Stinski MF;
XX WPI; 1992-424148/51.
XX Plasmids and DNA for transforming host cells - contain human
PT cytomegalovirus immediate-early, promoter-regulatory DNA sequence.
XX Claim 3; Fig 3; 5pp; English.
XX The sequence represents a consensus 16 base pair repeat found in the
CC human cytomegalovirus promoter regulatory region of the major immediate
CC early gene, representing the nucleotides most frequently found within the
CC 16n repeat. The promoter region contains the typical TATA and CAAT boxes
CC and three different sets of repeat sequences, designated 19n, 18n and 16n
CC repeats. Each repeat sequence is repeated at least 4 times. There is a
CC 21n repeat sequence which is repeated twice. The repeat sequence and/or
CC the surrounding sequences play a critical role in the relative level of
CC expression of the downstream gene. Experiments using various deletions of
CC the regulatory sequence suggest a direct correlation between the number
CC of repeats and the relative level of gene expression. Hence these
CC sequences or adjacent sequences constitute a component of the regulatory
CC region that enhances the level of expression of the adjacent gene. These
CC components are referred to as enhancers or activators. See also AAQ32183-
CC 95 and AAQ32430-4. (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 16 BP; 5 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 15.3%; Score 11.8; DB 1; Length 16;
Best Local Similarity 86.7%; Pred. No. 98;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 63 TGATGTCCTGTCAAG 77
DB 15 TGATGTCCTGTCAAG 1


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PR 05-OCT-1988; 88US-00256134.
PR 10-SEP-1990; 90US-00582130.
PA (IOWA ) UNIV IOWA STATE RES FOUND INC.
XX Stinski MF;
PI
XX WPI; 1995-081566/11.
DR
XX New transfer vectors for gene expression - comprising the immediate-early
PT promoter regulatory region of human cytomegalovirus.
XX
XX Disclosure; Fig 3; 10pp; English.
XX
XX The HCMV immediate-early promoter regulatory (IEPR) region, shown in
CC AAQ81478, enhances the transcription and expression of adjacent genes in
CC human cells, and has been used to construct gene transfer vector pIEPR12
CC (NRRL B-15930). The IEPR region includes 19n, 18n and 16n repeat sets,
CC each repeated 4 times, and a 21n set repeated twice. The 16n set is given
CC in AAQ81491-94, with the consensus in AAQ81490. (Updated on 25-MAR-2003
CC to correct PF field.)
XX
XX Sequence 16 BP; 5 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
SQ
    Query Match      15.3%; Score 11.8; DB 1; Length 16;
    Best Local Similarity 86.7%; Pred. No. 98;
    Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 63 TGATGTCCTGTCGAAG 77
Db 15 TGATGTACTGCCAAG 1

RESULT 122
AAV26760/c
ID AAV26760 standard; DNA; 16 BP.
XX
XX AAV26760;
AC
XX
XX 24-SEP-1998 (first entry)
DT
XX Human cytomegalovirus immediate-early promoter fusion site 16.
DE
XX ss; gag; gene delivery; pol; env; murine leukaemia virus; gene therapy.
XX
XX Synthetic.
OS
XX WO9812338-A1.
XX
XX 26-MAR-1998.
PD
XX
XX 22-SEP-1997; 97WO-KR000180.
PF
XX
XX 21-SEP-1996; 96KR-00041438.
XX
XX (VIRO-) VIROMEDICA PACIFIC LTD.
PA
XX Kim S, Kim S, Robbins PD;
PI
XX WPI; 1998-217273/19.
XX
XX New retroviral vectors, particularly for gene therapy - which are free of
PT the gag coding sequence, to provide for high levels of gene expression,
PT viral titre and packaging efficiency.
XX
XX Disclosure; Fig 7; 79pp; English.
PS
XX
XX The fusion sites AAV26756-V26760 were used in the production of two
CC retroviral vectors (RV). The first is a RV that has no gag coding
CC sequence is capable of delivering a gene of interest to a target cell
CC when packaging functions of gag, pol and env are provided. The second is
CC a RV based on murine leukaemia virus (MLV) where entire gag and env
CC coding sequences are completely deleted. The vectors can be used for gene

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CC therapy, for example for the delivery of hormones, enzymes, receptors or
CC drugs
XX
XX Sequence 16 BP; 5 A; 4 C; 3 G; 4 T; 0 U; 0 Other;
SQ
    Query Match      15.3%; Score 11.8; DB 1; Length 16;
    Best Local Similarity 86.7%; Pred. No. 98;
    Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 63 TGATGTCCTGTCGAAG 77
Db 15 TGATGTACTGCCAAG 1

RESULT 123
ABK72351/c
ID ABK72351 standard; DNA; 15 BP.
XX
XX ABK72351;
AC
XX
XX 30-JUL-2002 (first entry)
DT
XX Human HTR5A gene allele-specific oligonucleotide probe #13.
DE
XX
XX Human; 5-hydroxytryptamine receptor 5A; HTR5A; serotonin; probe; ss;
KW neuroprotective; neurological disease; depression; epilepsy;
KW gene therapy; single nucleotide polymorphism; haplotype pair;
KW chromosome 7q36.1.
XX
XX Homo sapiens.
OS
XX WO200222887-A1.
XX
XX 21-MAR-2002.
PD
XX
XX 17-SEP-2001; 2001WO-US029210.
PF
XX
XX 15-SEP-2000; 2000US-0233051P.
XX
XX (GENA-) GENAISANCE PHARM INC.
PA
XX Kazemi A, Koshy B, Sanchis A, Tirrell C;
PI
XX WPI; 2002-393978/42.
XX
XX Novel genetic variants of 5-Hydroxytryptamine (Serotonin) Receptor 5A
PT isogenes, useful for improving efficiency and reliability in drug
PT development for treating neurological diseases.
XX
XX Claim 17; Page 14; 134pp; English.
PS
XX
XX The invention relates to single nucleotide polymorphisms in the gene
CC encoding human 5-hydroxytryptamine (serotonin) receptor 5A (HTR5A). A
CC method for haplotyping the HTR5A gene in an individual comprises
CC identifying the nucleotide at one or more polymorphic sites and
CC determining whether one of the copies of the gene is defined by one of
CC the HTR5A haplotypes given in the specification or whether both copies
CC are defined by a haplotype pair. This method is useful in genotyping,
CC whereby all possible haplotype pairs can be assigned to specific
CC genotypes. An association between a trait and a haplotype or haplotype
CC pair of the HTR5A gene can be identified by comparing the frequency of
CC the frequency of the haplotype or haplotype pair in a reference
CC population, where a higher haplotype frequency in the trait population
CC indicates the trait is associated with the haplotype or haplotype pair.
CC HTR5A and its corresponding DNA are used for studying the expression and
CC function of HTR5A, and in screening for candidate drugs to treat diseases
CC related to HTR5A activity, such as neurological disorders, including
CC depression and epilepsy. Sequences ABK72339-ABK72358 represent allele-
CC specific oligonucleotide probes used for detecting HTR5A gene
CC polymorphisms
XX
XX Sequence 15 BP; 2 A; 8 C; 2 G; 2 T; 0 U; 1 Other;
SQ

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Query Match      15.1%; Score 11.6; DB 1; Length 15;
Best Local Similarity 91.7%; Pred. No. 98;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGCTGGGGGATA 22
Db 12 GGCCWGGGGATA 1

RESULT 124
ABF84445/c
ID ABF844445 standard; DNA; 13 BP.
XX AC ABF844445;
XX XX
DT 22-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 184442 for detecting SNP TSC0045516.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
OS Homo sapiens.
XX XX
FN WO200177384-A2.
XX XX
PD 18-OCT-2001.
XX XX
DT 22-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 184442 for detecting SNP TSC0045516.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
OS Homo sapiens.
XX XX
FN WO200177384-A2.
XX XX
PD 18-OCT-2001.
XX XX
DT 06-APR-2001; 2001WO-IB000713.
XX XX
PR 07-APR-2000; 2000DE-01019173.
XX XX
PA (BPIG-) EPIGENOMICS AG.
XX XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX
PS Claim 1; SEQ ID NO 184442; 29pp + Sequence Listing; German.
XX XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX
SQ Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;
XX XX
Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 90;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGCTAAGA 51
Db 13 TGAGATGTAAGA 1

RESULT 125
ABC41770
ID ABC41770 standard; DNA; 13 BP.

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XX AC ABC41770;
XX XX
DT 21-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 41787 for detecting SNP TSC0012525.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
OS Homo sapiens.
XX XX
FN WO200177384-A2.
XX XX
PD 18-OCT-2001.
XX XX
DT 06-APR-2001; 2001WO-IB000713.
XX XX
PR 07-APR-2000; 2000DE-01019173.
XX XX
PA (BPIG-) EPIGENOMICS AG.
XX XX
PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX XX
PS Claim 1; SEQ ID NO 41787; 29pp + Sequence Listing; German.
XX XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX XX
SQ Sequence 13 BP; 5 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
XX XX
Query Match      14.8%; Score 11.4; DB 1; Length 13;
Best Local Similarity 92.3%; Pred. No. 90;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGCTAAGA 51
Db 1 TGAGAGGCTAAGA 13

RESULT 126
ABF84444
ID ABF844444 standard; DNA; 13 BP.
XX XX
AC ABF844444;
XX XX
DT 22-FEB-2002 (first entry)
XX XX
DE Oligonucleotide SEQ ID NO 184441 for detecting SNP TSC0045516.
XX XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX XX
OS Homo sapiens.
XX XX

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PN WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 184441; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 14.8%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 90;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 39 TGAGAGGTTAAGA 51
XX DB 1 TGAGATGTTAAGA 13
XX
XX RESULT 127
XX ABC4171/c
XX ID ABC41771 standard; DNA; 13 BP.
XX
XX AC ABC41771;
XX
XX 21-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 41788 for detecting SNP TSC0012525.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 41788; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Query Match 14.8%; Score 11.4; DB 1; Length 13;
XX Best Local Similarity 92.3%; Pred. No. 90;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 39 TGAGAGGTTAAGA 51
XX DB 1 TGAGATGTTAAGA 13
XX
XX RESULT 128
XX AAN70550
XX ID AAN70550 standard; DNA; 14 BP.
XX
XX AC AAN70550;
XX
XX 25-MAR-2003 (revised)
XX 29-APR-1991 (first entry)
XX
XX Sequence of probe for human tissue plasminogen activator (TPA) gene.
XX
XX Thrombolytic; enzyme; protease; ss.
XX
XX Homo sapiens.
XX
XX EP211260-A.
XX
XX 25-FEB-1987.
XX
XX 09-JUL-1986; 86EP-00109385.
XX
XX 10-JUL-1985; 85JP-00152810.
XX 31-JAN-1986; 86JP-00020469.
XX 26-APR-1986; 86JP-00097481.
XX
XX (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.
XX (KANF-) KANEGAFUCHI.
XX
XX Kakutani T, Matsumoto K, Yahara H, Maruyama H, Kawaharada H;
XX Watanabe K;
XX WPI; 1987-051507/08.
XX
XX New chromosomal DNA coding for human tissue plasminogen activator -
XX useful in expression vectors for high yield prodn. of activator by large
XX scale suspension culture.
XX
XX Example; p24; 70pp; English.
XX
XX The probe is used in an example to exemplify the cloning of TPA gene.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX

```


SQ Sequence 14 BP; 2 A; 4 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 14.8%; Score 11.4; DB 1; Length 14;
 Best Local Similarity 92.3%; Pred. No. 98;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 60 AGCTGATGCTCTGG 72
 DB 2 AGCTGATGCCCTG 14
 |||||
 |||||

RESULT 129
 AAF48760
 ID AAF48760 standard; DNA; 15 BP.
 XX AC
 XX AAF48760;
 XX 30-MAR-2001 (first entry)
 XX DE IGFBP3 oligonucleotide #2180.
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX OS Homo sapiens.
 XX PN WO200078341-A1.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX PI Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX PS Example 7; Page 58; 201pp; English.
 XX CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX SQ Sequence 15 BP; 4 A; 4 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 1.1e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GATACAACTCTGG 31
 |||||
 |||||

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 130
 AAF48758
 ID AAF48758 standard; DNA; 15 BP.
 XX AC
 XX AAF48758;
 XX 30-MAR-2001 (first entry)
 XX DE IGFBP3 oligonucleotide #2178.
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytosolic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX OS Homo sapiens.
 XX PN WO200078341-A1.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX PI Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX PS Example 7; Page 58; 201pp; English.
 XX CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX SQ Sequence 15 BP; 5 A; 2 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;
 Best Local Similarity 92.3%; Pred. No. 1.1e+02;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 19 GATACAACTCTGG 31
 |||||
 |||||

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Db      3  GATACAACTGTGG 15
RESULT 131
AAF48759
ID  AAF48759 standard; DNA; 15 BP.
XX
XX  AAF48759;
XX
XX  30-MAR-2001 (first entry)
XX
XX  IGFBP3 oligonucleotide #2179.
XX
XX  Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX  cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
XX  skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX  IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX  growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
XX  keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX  hyperneovascular condition; hyperplasia; kidney disease;
XX  neovascular condition of the retina; ss.
XX
XX  Homo sapiens.
XX
XX  WO200078341-A1.
XX
XX  28-DEC-2000.
XX
XX  21-JUN-2000; 2000WO-AU000693.
XX
XX  21-JUN-1999; 99US-0140345P.
XX
XX  (MURD-) MURDOCH CHILDRENS RES INST.
XX
XX  Wraight CJ, Werther GA, Edmondson SR;
XX
XX  WPI; 2001-041421/05.
XX
XX  Ameliorating the effects of a disorder, e.g. psoriasis, by administering
XX  UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
XX  inhibits or reduces growth factor mediated cell proliferation and/or
XX  inflammation.
XX
XX  Example 7; Page 58; 201pp; English.
XX
XX  The present invention relates to a method for ameliorating the effects of
XX  skin disorders. The method comprises contacting the skin with an
XX  antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
XX  receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
XX  inhibiting or reducing growth factor mediated cell proliferation,
XX  inflammation and/or other disorders. The present sequence is an
XX  oligonucleotide which can be used to design the antisense
XX  oligonucleotides of the present invention (see AAF45151 and AAF45153-
XX  F45161). The method is useful for ameliorating the effects of psoriasis,
XX  ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
XX  neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
XX  hyperneovascular condition such as a neovascular condition of the retina,
XX  brain or skin, growth factor-mediated malignancies, other sclerotic
XX  disease, kidney disease, hyperproliferation of the inside of blood
XX  vessels or any other hyperplasia
XX
XX  Sequence 15 BP; 4 A; 3 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX  Query Match 14.8%; Score 11.4; DB 1; Length 15;
XX  Best Local Similarity 92.3%; Pred. No. 1.1e+02;
XX  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX  Qy 19 GATACAACTGTGG 31
XX  Dd 2 GATACAACTGTGG 14
XX
RESULT 132

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ADV37029
ID  ADV37029 standard; RNA; 15 BP.
XX
XX  ADV37029;
XX
XX  10-FEB-2005 (first entry)
XX
XX  Human anti-HER2 NCH ribozyme substrate sequence #908.
XX
XX  Enzymatic nucleic acid molecule; gene expression; down regulation;
XX  protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
XX  MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
XX  beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
XX  c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
XX  hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
XX  amberzyme; zinyne; DNazyme; cancer; breast cancer; Alzheimer's disease;
XX  diabetes; obesity; cardiac disease; heart disease; age-related disease;
XX  hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
XX  ss.
XX
XX  Homo sapiens.
XX
XX  WO200116312-A2.
XX
XX  08-MAR-2001.
XX
XX  30-AUG-2000; 2000WO-US023998.
XX
XX  31-AUG-1999; 99US-0151713P.
XX  27-SEP-1999; 99US-00406643.
XX  27-SEP-1999; 99US-0156236P.
XX  27-SEP-1999; 99US-0156467P.
XX  08-NOV-1999; 99US-00436430.
XX  06-DEC-1999; 99US-0169100P.
XX  29-DEC-1999; 99US-00474432.
XX  29-DEC-1999; 99US-0173612P.
XX  30-DEC-1999; 99US-00476387.
XX  04-FEB-2000; 2000US-00498824.
XX  20-MAR-2000; 2000US-00531025.
XX  14-APR-2000; 2000US-0197769P.
XX  23-MAY-2000; 2000US-00578223.
XX  09-AUG-2000; 2000US-00636385.
XX
XX  (RIBO-) RIBOZYME PHARM INC.
XX
XX  Mcswiggen J, Usman N, Blatt L, Reigelman L, Burgin A;
XX  Karpeisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
XX  Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
XX  WPI; 2001-244406/25.
XX
XX  Enzymatic nucleic acid molecules able to cleave separate RNA molecules
XX  are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
XX  obesity and heart disease.
XX
XX  Example 7; Page 490; 717pp; English.
XX
XX  The present invention relates to the use of enzymatic nucleic acid
XX  molecules (e.g. ribozymes) to modulate gene expression. The invention of
XX  also methods for their use to down regulate or inhibit the expression of
XX  genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
XX  aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
XX  alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
XX  receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
XX  presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
XX  nucleic acid molecules used to inhibit the expression of the said genes
XX  include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
XX  zinyne, and/or DNazyme motifs. The methods of the invention are useful
XX  for treating cancer, in particular breast cancer, Alzheimer's disease,
XX  diabetes, obesity, cardiac diseases e.g. heart disease, age-related
XX  diseases, hepatitis B infections, and hepatitis and hepatocellular
XX  carcinoma. The enzymatic nucleic acid molecules can also be used as
XX  diagnostic tools to examine genetic drift and mutations within diseased

```

CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a substrate/target sequence for an anti-HER2 NCH
 CC ribozyme used in the examples of the present invention. Note: Some SEQ ID
 CC Nos are repeated more than once in the specification, but these have
 CC different sequences associated with them.

XX Sequence 15 BP; 3 A; 4 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;

Best Local Similarity 69.2%; Pred. No. 1.1e+02;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 29 TGGAGTCTCTGGA 41

Db 1 UGGAGCCUCUGA 13

RESULT 133

AAL48040

ID AAL48040 standard; DNA; 15 BP.

XX AC

XX AAL48040;

XX 27-SEP-2002 (first entry)

XX Human CSF3 gene allele specific primer SEQ ID NO: 18.

XX DE

XX Human; colony stimulating factor 3 (granulocyte); CSF3; SNP; isogene;

XX chromosome 17q11-12; single nucleotide polymorphism; immunostimulant;

XX neutropenia; promyelocytic leukaemia; haematological disorder;

XX gene therapy; PCR; primer; ss.

XX OS

XX Homo sapiens.

XX WO200194364-A2.

XX 13-DEC-2001.

XX 11-JUN-2001; 2001WO-US018913.

XX 09-JUN-2000; 2000US-0210380P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Duda A, Kazemi A, Messer C, Sausker EA;

XX WPI; 2002-566435/60.

XX New variants of colony stimulating factor 3 (CSF3) isogenes, useful for
 PT improving efficiency and reliability in the development of drugs for
 PT treating diseases associated with CSF3 activity e.g. neutropenia.

PS Claim 17; Page 13; 68pp; English.

XX The present invention provides the protein, gene and cDNA sequences of
 CC human colony stimulating factor 3 (granulocyte) CSF3. Also described are
 CC single nucleotide polymorphisms (SNPs) identified within these sequences.
 CC The sequences can be used in the treatment of neutropenia, promyelocytic
 CC leukaemia and haematological disorders. The present sequence is an allele
 CC specific primer used to isolate the coding sequences of the invention

XX Sequence 15 BP; 2 A; 1 C; 9 G; 2 T; 0 U; 1 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 AGACGGCTGGGGAT 21

Db 1 AGAGGGGCTGGGGRT 15

RESULT 134

ABN80560/C

ID ABN80560 standard; DNA; 15 BP.

XX AC

XX ABN80560;

XX 19-JUL-2002 (first entry)

XX Human P450(cytochrome) oxidoreductase allele specific probe #26.

XX Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;

XX single nucleotide polymorphism; flavoprotein; enzyme; probe; ss.

XX OS

XX Homo sapiens.

XX WO200226768-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-US030877.

XX 29-SEP-2000; 2000US-0236449P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Kazemi A, Kliem SE, Lanz EM, Messer C, Tanguay DA;

XX WPI; 2002-394236/42.

XX New genetic variants comprising haplotypes of the P450 (cytochrome)
 PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug
 PT screening protocols for compounds targeting POR.

XX Claim 14; Page 14; 141pp; English.

XX The present invention provides the protein, gene and cDNA sequences of
 CC human P450(cytochrome) oxidoreductase POR, and single nucleotide
 CC polymorphisms (SNPs) identified therein. The sequences can be used to
 CC haplotype the POR gene of an individual, and to establish whether POR is
 CC a suitable target for drugs to treat cancer and disorders associated with
 CC impaired protein synthesis in cells. The present sequence is an allele
 CC specific probe for the coding sequences of the invention

XX Sequence 15 BP; 1 A; 6 C; 3 G; 4 T; 0 U; 1 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAAGCTGA 65

Db 15 AGCCAGCGGAGCTGA 1

RESULT 135

ADJ82348

ID ADJ82348 standard; DNA; 15 BP.

XX AC

XX ADJ82348;

XX 06-MAY-2004 (first entry)

XX KLM5Y-encoding nucleotide #76.

XX ss; cytotstatic; platelet-derived growth factor receptor; PDGFR; cancer;

XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;

XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;

XX myeloproliferative disease; blood vessel proliferative disease;

XX angiogenesis.

XX OS

XX Synthetic.

XX WO2003045973-A2.

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PD 05-JUN-2003.
XX
XX 30-SEP-2002; 2002WO-US031165.
XX
XX 28-NOV-2001; 2001US-0333476P.
XX
XX (BECT ) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX Dean C, Heidaran M, Spargo CA;
XX WPI; 2003-505179/47.
XX
XX New peptides having growth inhibitory action, useful for inhibiting tumor
XX or cancer cell proliferation, or for treating fibrotic disorders,
XX myeloproliferative diseases, and blood vessel proliferative (angiogenic)
XX disorders.
XX
XX Disclosure; SEQ ID NO 129; 48pp; English.
XX
XX The invention relates to an isolated peptide or polypeptide (I) of no
XX more than about 50 amino acid residues which when contacted with cells in
XX which a platelet-derived growth factor receptor (PDGF-R) is activated in
XX an autocrine manner, inhibits the growth of these cells. The isolated
XX peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
XX Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
XX Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
XX proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
XX sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
XX or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
XX ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
XX muscle or bone cell. The peptides are also useful for treating fibrotic
XX disorders, myeloproliferative diseases, and blood vessel proliferative
XX (angiogenic) disorders. This sequence represents a possible nucleotide
XX encoding the P3 peptide.
XX
XX Sequence 15 BP; 4 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 14.8%; Score 11.4; DB 1; Length 15;
XX Best Local Similarity 92.3%; Pred. No. 1.1e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 59 AAGCTGATGTCCT 71
XX ||||| |||||
XX 1 AAGCTTATGTCCT 13
XX
XX RESULT 136
XX ADJ82364
XX ID ADJ82364 standard; DNA; 15 BP.
XX
XX AC ADJ82364;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE KLMSY-encoding nucleotide #92.
XX
XX SS; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
XX myeloproliferative disease; blood vessel proliferative disease;
XX angiogenesis.
XX
XX OS Synthetic.
XX
XX WO2003045973-A2.
XX
XX PD 05-JUN-2003.
XX
XX PF 30-SEP-2002; 2002WO-US031165.
XX
XX PR 28-NOV-2001; 2001US-0333476P.
XX
XX (BECT ) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX Dean C, Heidaran M, Spargo CA;
XX WPI; 2003-505179/47.
XX
XX New peptides having growth inhibitory action, useful for inhibiting tumor
XX or cancer cell proliferation, or for treating fibrotic disorders,
XX myeloproliferative diseases, and blood vessel proliferative (angiogenic)
XX disorders.
XX
XX Disclosure; SEQ ID NO 129; 48pp; English.
XX
XX The invention relates to an isolated peptide or polypeptide (I) of no
XX more than about 50 amino acid residues which when contacted with cells in
XX which a platelet-derived growth factor receptor (PDGF-R) is activated in
XX an autocrine manner, inhibits the growth of these cells. The isolated
XX peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
XX Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
XX Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (I) is useful for inhibiting cell
XX proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
XX sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
XX or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
XX ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
XX muscle or bone cell. The peptides are also useful for treating fibrotic
XX disorders, myeloproliferative diseases, and blood vessel proliferative
XX (angiogenic) disorders. This sequence represents a possible nucleotide
XX encoding the P3 peptide.
XX
XX Sequence 15 BP; 4 A; 4 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 14.8%; Score 11.4; DB 1; Length 15;
XX Best Local Similarity 92.3%; Pred. No. 1.1e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 59 AAGCTGATGTCCT 71
XX ||||| |||||
XX 1 AAGCTTATGTCCT 13
XX
XX RESULT 137
XX ADJ82388
XX ID ADJ82388 standard; DNA; 15 BP.
XX
XX AC ADJ82388;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE KLMSY-encoding nucleotide #116.
XX
XX SS; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
XX carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
XX neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
XX myeloproliferative disease; blood vessel proliferative disease;
XX angiogenesis.
XX
XX OS Synthetic.
XX
XX WO2003045973-A2.
XX
XX PD 05-JUN-2003.
XX
XX PF 30-SEP-2002; 2002WO-US031165.
XX
XX PR 28-NOV-2001; 2001US-0333476P.
XX
XX (BECT ) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX Dean C, Heidaran M, Spargo CA;
XX WPI; 2003-505179/47.
XX

```

XX New peptides having growth inhibitory action, useful for inhibiting tumor
PT or cancer cell proliferation, or for treating fibrotic disorders,
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
PT disorders.

XX Disclosure; SEQ ID NO 169; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no
CC more than about 50 amino acid residues which when contacted with cells in
CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
CC an autocrine manner, inhibits the growth of these cells. The isolated
CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell
CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
CC muscle or bone cell. The peptides are also useful for treating fibrotic
CC disorders, myeloproliferative diseases, and blood vessel proliferative
CC (angiogenic) disorders. This sequence represents a possible nucleotide
CC encoding the P3 peptide.

XX Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71
DB 1 AAGCTGATGTCCT 13

RESULT 138
ADJ82334
ID ADJ82394 standard; DNA; 15 BP.
XX
AC ADJ82394;
XX
DT 06-MAY-2004 (first entry)
XX
DB KLMXY-encoding nucleotide #122.
XX
XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
KW myeloproliferative disease; blood vessel proliferative disease;
KW angiogenesis.
XX
XX Synthetic.
XX WO2003045973-A2.
XX
XX 05-JUN-2003.
XX
XX 30-SEP-2002; 2002WO-US031165.
XX
XX 28-NOV-2001; 2001US-0333476P.
XX
XX (SECT) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX Dean C, Heidaran M, Spargo CA;
XX WPI; 2003-505179/47.
XX
XX New peptides having growth inhibitory action, useful for inhibiting tumor
PT or cancer cell proliferation, or for treating fibrotic disorders,
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
PT disorders.

PS Disclosure; SEQ ID NO 175; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no
CC more than about 50 amino acid residues which when contacted with cells in
CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
CC an autocrine manner, inhibits the growth of these cells. The isolated
CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-
CC Lys (P1) Asp-Asp-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-
CC Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5). (I) is useful for inhibiting cell
CC proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma,
CC sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma,
CC or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,
CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain,
CC muscle or bone cell. The peptides are also useful for treating fibrotic
CC disorders, myeloproliferative diseases, and blood vessel proliferative
CC (angiogenic) disorders. This sequence represents a possible nucleotide
CC encoding the P3 peptide.

XX Sequence 15 BP; 4 A; 3 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71
DB 1 AAGCTGATGTCCT 13

RESULT 139
ADJ82380
ID ADJ82380 standard; DNA; 15 BP.
XX
AC ADJ82380;
XX
DT 06-MAY-2004 (first entry)
XX
DB KLMXY-encoding nucleotide #108.
XX
XX ss; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer;
KW carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma;
KW neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders;
KW myeloproliferative disease; blood vessel proliferative disease;
KW angiogenesis.
XX
XX Synthetic.
XX WO2003045973-A2.
XX
XX 05-JUN-2003.
XX
XX 30-SEP-2002; 2002WO-US031165.
XX
XX 28-NOV-2001; 2001US-0333476P.
XX
XX (SECT) BECTON DICKINSON & CO.
XX (HAAL/) HAALAND P D.
XX
XX Dean C, Heidaran M, Spargo CA;
XX WPI; 2003-505179/47.
XX
XX New peptides having growth inhibitory action, useful for inhibiting tumor
PT or cancer cell proliferation, or for treating fibrotic disorders,
PT myeloproliferative diseases, and blood vessel proliferative (angiogenic)
PT disorders.

XX Disclosure; SEQ ID NO 161; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (I) of no
CC more than about 50 amino acid residues which when contacted with cells in
CC which a platelet-derived growth factor receptor (PDGF-R) is activated in
CC an autocrine manner, inhibits the growth of these cells. The isolated

CC peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (1) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.

XX
SQ Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. NO. 1.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71
||||| |||||
Db 1 AAGCTGATGTCCT 13

RESULT 140
ADJ82332
ID ADJ82332 standard; DNA; 15 BP.

XX AC ADJ82332;

DT 06-MAY-2004 (first entry)

XX DE KLMSY-encoding nucleotide #60.

XX SS; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; angiogenesis.

XX OS Synthetic.

XX PN WO2003045973-A2.

XX PD 05-JUN-2003.

XX PF 30-SEP-2002; 2002WO-US031165.

XX PR 28-NOV-2001; 2001US-0333476P.

XX PA (BECT) BECTON DICKINSON & CO.
(HAAL/) HAALAND P D.

XX PI Dean C, Heidaran M, Spargo CA;

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, PT myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.

XX PS Disclosure; SEQ ID NO 113; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (1) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (1) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney,

CC ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.

XX SQ Sequence 15 BP; 5 A; 4 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 14.8%; Score 11.4; DB 1; Length 15;
Best Local Similarity 92.3%; Pred. NO. 1.1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 59 AAGCTGATGTCCT 71
||||| |||||
Db 1 AAGCTGATGTCCT 13

RESULT 141

ADJ82398

ID ADJ82398 standard; DNA; 15 BP.

XX AC ADJ82398;

XX DT 06-MAY-2004 (first entry)

XX DE KLMSY-encoding nucleotide #126.

XX SS; cytostatic; platelet-derived growth factor receptor; PDGF-R; cancer; carcinoma; sarcoma; osteosarcoma; glioma; melanoma; myxoma; adenoma; neuroblastoma; rhabdomyoma-derived cell; fibrotic disorders; myeloproliferative disease; blood vessel proliferative disease; angiogenesis.

XX OS Synthetic.

XX PN WO2003045973-A2.

XX PD 05-JUN-2003.

XX PF 30-SEP-2002; 2002WO-US031165.

XX PR 28-NOV-2001; 2001US-0333476P.

XX PA (BECT) BECTON DICKINSON & CO.
(HAAL/) HAALAND P D.

XX PI Dean C, Heidaran M, Spargo CA;

XX WPI; 2003-505179/47.

XX New peptides having growth inhibitory action, useful for inhibiting tumor or cancer cell proliferation, or for treating fibrotic disorders, PT myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders.

XX PS Disclosure; SEQ ID NO 179; 48pp; English.

XX The invention relates to an isolated peptide or polypeptide (1) of no more than about 50 amino acid residues which when contacted with cells in which a platelet-derived growth factor receptor (PDGF-R) is activated in an autocrine manner, inhibits the growth of these cells. The isolated peptides or polypeptides preferably have the sequences: Lys-Lys-Lys-Lys-Lys (P1) Asp-Asp-Glu-Glu-Lys (P2) Lys-Leu-Met-Ser-Tyr (P3) Phe-Phe-Lys-Lys (P4) Phe-Phe-His-Pro-Val (P5) . (1) is useful for inhibiting cell proliferation, where the cell is a tumor or cancer cell (e.g. carcinoma, sarcoma, osteosarcoma, glioma, melanoma, myxoma, adenoma, neuroblastoma, or rhabdomyoma-derived cell), lung, breast, colon, prostate, kidney, ovary, testicular, skin, pancreatic, thyroid, adrenal, pituitary, brain, muscle or bone cell. The peptides are also useful for treating fibrotic disorders, myeloproliferative diseases, and blood vessel proliferative (angiogenic) disorders. This sequence represents a possible nucleotide encoding the P3 peptide.

Db 15 GATACNGCTCTNGAG 1

RESULT 144

ADL13694/C
ID ADE13694 standard; DNA; 16 BP.

XX AC ADE13694;

XX DT 29-JAN-2004 (first entry)

XX DE Oligonucleotide probe for diagnostic purposes seq id 26.

XX KW polymorphism detection; diagnostic;
KW single nucleotide polymorphism detection; SNP detection; array technology;
KW sequencing; hybridisation; ss; probe.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX modified_base 4

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= Not described"

FT modified_base 10

FT /*tag= b

FT /mod_base= OTHER

FT /note= "OTHER= Not described"

XX US2003170711-A1.

XX PN 11-SEP-2003.

XX PD 25-FEB-2003; 2003US-00375504.

XX PF 02-OCT-1997; 97US-0060673P.

XX PR 18-AUG-1998; 98US-00136080.

XX PR 18-JUL-2001; 2001US-0306229P.

XX PR 08-MAY-2002; 2002US-00142729.

XX (BROW/) BROWN B D.

PA (RILE/) RILEY T A.

XX Brown BD, Riley TA;

XX WPI; 2003-830610/77.

XX New oligonucleotide for diagnostic purposes, e.g. detection of single

PT nucleotide polymorphisms, comprises universal and generic bases.

PS Disclosure; SEQ ID NO 26; 37pp; English.

XX The invention describes an oligonucleotide comprising 10-100 bases, in

CC which at least 2 bases are juxtaposed universal bases. Also disclosed is

CC a method for detecting a polymorphism in a genetic material comprising

CC contacting a DNA with the new oligonucleotide, and identifying whether

CC the oligonucleotide bound to the DNA. The novel oligonucleotide is used

CC for diagnostic purposes, e.g. detection of single nucleotide

CC polymorphisms (SNPs). It is also applicable in array technology,

CC sequencing, and hybridisation. The method increases the ability to

CC differentiate a single nucleotide polymorphism or a polymorphic site from

CC a normal site and allows the development of more efficient diagnostics

CC and therapeutics. This sequence represents an oligonucleotide of the

CC invention. Note: This sequence differs from the sequence given in the

XX examples of the invention.

SQ Sequence 16 BP; 3 A; 4 C; 3 G; 4 T; 0 U; 2 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 16;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX 19 GATACAACTCTGGAG 33

QY

Db 15 GATACNGCTCTNGAG 1

RESULT 145

ADM83304
ID ADM83304 standard; DNA; 16 BP.

XX AC ADM83304;

XX DT 03-JUN-2004 (first entry)

XX DE Probe 6 #2 used to identify mutations or polymorphisms.

XX KW Diagnosis; polymorphism detection; genetic disease; probe; ss.

XX OS Unidentified.

XX FH Key Location/Qualifiers

XX misc_feature 4..5

FT /*tag= a

FT /note= "Linked via 3 numbers of 3-nitropyrrole group"

FT misc_feature 12..13

FT /*tag= b

FT /note= "Linked via 2 numbers of 3-nitropyrrole group"

XX US2003165888-A1.

XX PN 04-SEP-2003.

XX PD 08-MAY-2002; 2002US-00142729.

XX PR 18-JUL-2001; 2001US-0306229P.

XX (BROW/) BROWN B D.

PA (RILE/) RILEY T A.

XX Brown BD, Riley TA;

XX WPI; 2003-787489/74.

XX New oligonucleotides useful as primers and probes for diagnosing

PT diseases, i.e. polymorphism in sample of genetic material, comprises

PT bases where some are juxtaposed universal bases.

PS Example 7; SEQ ID NO 35; 18pp; English.

XX The invention relates to novel oligonucleotide probes and primers

CC comprising universal and generic bases. The oligonucleotides of the

CC invention are useful as primers and probes for diagnosing diseases,

CC particularly in detecting polymorphism in a sample of genetic material

CC and for diagnosing a genetic disease in a patient. The present sequence is

CC a probe used to identify mutations or polymorphisms. This sequence is

CC used in the exemplification of the invention.

XX SQ Sequence 16 BP; 4 A; 4 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 14.8%; Score 11.4; DB 1; Length 16;

Best Local Similarity 92.3%; Pred. No. 1.1e+02;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 CTTCTGAGAGGTAA 48

DB 1 CTTCTGAGAGGTAA 13

RESULT 146

ADM83291

ID ADM83291 standard; DNA; 16 BP.

XX AC ADM83291;

XX DT 03-JUN-2004 (first entry)


```

XX DE Probe 6 #1 used to identify mutations or polymorphisms.
XX KW Diagnosis; polymorphism detection; genetic disease; probe; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX misc_feature 4..5
XX FT /*tag= a
XX FT /note= "Linked via 3 numbers of 3-nitropyrrrole group"
XX FT 15..16
XX FT /*tag= b
XX FT /note= "Linked via 2 numbers of 3-nitropyrrrole group"
XX US2003165888-A1.
XX PN
XX XX
XX PD 04-SEP-2003.
XX XX
XX PF 08-MAY-2002; 2002US-00142729.
XX XX
XX PR 18-JUL-2001; 2001US-0306229P.
XX XX
XX PA (BROW/) BROWN B D.
XX PA (RILE/) RILEY T A.
XX XX
XX PI Brown BD, Riley TA;
XX XX
XX DR WPI; 2003-787489/74.
XX XX
XX PT New oligonucleotides useful as primers and probes for diagnosing
XX PT diseases, i.e. polymorphism in sample of genetic material, comprises
XX PT bases where some are juxtaposed universal bases.
XX XX
XX PS Example 6; SEQ ID NO 22; 18pp; English.
XX XX
XX CC The invention relates to novel oligonucleotide probes and primers
XX CC comprising universal and generic bases. The oligonucleotides of the
XX CC invention are useful as primers and probes for diagnosing diseases,
XX CC particularly in detecting polymorphism in a sample of genetic material
XX CC and for diagnosing a genetic disease in a patient. The present sequence
XX CC is a probe used to identify mutations or polymorphisms. This sequence is
XX CC used in the exemplification of the invention.
XX XX
XX SQ Sequence 16 BP; 4 A; 4 C; 3 G; 5 T; 0 U; 0 Other;
XX XX
XX Query Match 14.8%; Score 11.4; DB 1; Length 16;
XX Best Local Similarity 92.3%; Pred. No. 1.1e+02;
XX Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX XX
XX Qy 36 CTCGTGAGAGGTAA 48
XX Db 1 CTCGTGAGAGGTAA 13
XX XX
XX RESULT 147
XX AAT18111
XX ID AAT18111 standard; DNA; 16 BP.
XX XX
XX AC AAT18111;
XX XX
XX DT 30-AUG-1996 (first entry)
XX XX
XX DE M. kansasii species specific amplification primer. DI.
XX XX
XX KW Species-specific amplification; M. kansasii; p6123; probe; pMK1-9;
XX KW strand displacement amplification; SDA; primers; Mycobacterium;
XX KW cross-react; Nocardia asteroides; Rhodococcus rhodochrous; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN US5500341-A.
XX XX

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PD 19-MAR-1996.
XX PF 19-SEP-1994; 94US-00308892.
XX PR 19-SEP-1994; 94US-00308892.
XX PA (BECT ) BECTON DICKINSON CO.
XX XX
XX PI Spears PA;
XX XX
XX DR WPI; 1996-171042/17.
XX XX
XX PT Primers for species-specific amplification of Mycobacterium kansasii -
XX PT detect double stranded target sequences with no cross-reactivity between
XX PT species.
XX XX
XX PS Disclosure; Col 17; 15pp; English.
XX XX
XX CC The sequences given in AAT18103-11 are primers which may be used in the
XX CC species-specific amplification of M. kansasii DNA. These primers bind to
XX CC a fragment, bases 51-220, of the clone p6123. p6123 is a cloned probe
XX CC which hybridises to all M. kansasii strains, including the subgroup which
XX CC is negative to binding with the probe pMK1-9 (M.Yang et al. 1993. J.
XX CC Clin. Microbid. 31, 2769-2772). These primers are pref. used in strand
XX CC displacement amplification (SDA). These primers showed a positive
XX CC reaction with 74 M. kansasii isolates tested, but did not cross react
XX CC with any other Mycobacterium species. In addition, these primers did not
XX CC cross-react with Nocardia asteroides or Rhodococcus rhodochrous. This
XX CC primer binds around bases 141-156 of the p6123 fragment
XX XX
XX SQ Sequence 16 BP; 3 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX XX
XX Query Match 14.5%; Score 11.2; DB 1; Length 16;
XX Best Local Similarity 81.2%; Pred. No. 1.2e+02;
XX Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX XX
XX Qy 3 AACAGACGCGCCTGGG 18
XX Db 1 AACTCGACGCGCCTCGG 16
XX XX
XX RESULT 148
XX ABS56009/C
XX ID ABS56009 standard; RNA; 16 BP.
XX XX
XX AC ABS56009;
XX XX
XX DT 07-AUG-2003 (revised)
XX DT 07-JAN-2003 (first entry)
XX XX
XX DE West Nile virus genome, nucleotides 1-16.
XX XX
XX KW Mutant replication-defective flavivirus; arthropod vector;
XX KW 3' stem-loop structure substitution; Dengue virus type 2; DEN2;
XX KW West Nile virus; WN; flavivirus-induced infection; dengue fever;
XX KW dengue haemorrhagic fever; dengue shock syndrome; virucide; ss.
XX XX
XX OS West Nile virus.
XX XX
XX PN WO200274963-A1.
XX XX
XX PD 26-SEP-2002.
XX XX
XX PF 16-MAR-2001; 2001WO-US008686.
XX XX
XX PR 16-MAR-2001; 2001WO-US008686.
XX XX
XX PA (USSH ) US DEPT OF HEALTH.
XX XX
XX PI Markoff L, Zeng L;
XX XX
XX DR WPI; 2002-750556/81.
XX XX

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PT New mutant replicon-defective flavivirus having a genome with a 3' stem-
 PT loop structure chimeric substitution useful as vaccine for treating
 PT flavivirus-induced infection e.g. dengue fever, dengue hemorrhagic
 PT fever/shock syndrome.

XX Example 3; Page 61; 67pp; English.

PS The present invention relates to a mutant replication-defective
 XX flavivirus having a genome with a 3' stem-loop structure substitution,
 CC and being defective for replication in an arthropod vector that transmits
 CC flavivirus to humans. The genome is selected from a first flavivirus and
 CC the 3' stem-loop structure from a second flavivirus, where the first
 CC flavivirus is different from the second. For example the first flavivirus
 CC may be Dengue virus type 2 (DENV2) and the second flavivirus may be West
 CC Nile virus (WNV). The mutant replicon-defective flavivirus is useful as a
 CC vaccine for treating flavivirus-induced infections, particularly dengue
 CC fever or dengue haemorrhagic fever/shock syndrome. The present sequence
 CC represents a part of the WNV genome used to construct a mutant replication
 CC -defective flavivirus in the examples of the present invention. (Updated
 CC on 07-AUG-2003 to correct OS field.)

XX Sequence 16 BP; 7 A; 3 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 14.5%; Score 11.2; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 1.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 26 CTCTGGAGTCTCTGA 41

Db 16 CTCTGTGTCTCTATGA 1

RESULT 149

ABK29916/c
 ID ABK29916 standard; DNA; 16 BP.

XX ABK29916;

XX 23-APR-2002 (first entry)

XX Androgen receptor wild type HLH-3 sequence.

XX Cyclin D1 promoter; CD40L promoter; hepatitis B virus promoter;
 KW HBV promoter; vancomycin-resistant enterococci promoter; VRE promoter;
 KW vanH promoter; androgen receptor promoter; AR promoter;
 KW human epidermal growth factor receptor 2 promoter; her2 promoter;
 KW beta lactamase promoter; Bla promoter; transgene; cancer; breast cancer;
 KW colon cancer; immunological disorder; prostate cancer; cytostatic;
 KW autoimmune disease; HBV pre-S promoter; HBV-X promoter;
 KW enterococcus infection; immunosuppressive; antibacterial; antiviral;
 KW gene expression modulator; multiple sclerosis; MS;
 KW chronic hepatic insufficiency; cirrhosis; hepatocellular carcinoma;
 KW systematic lupus erythematosus; SLE; graft-vs-host disease; GVHD;
 KW familial adenomatous polyposis; rheumatoid arthritis; PCR; primer;
 KW transgenic; ss.

XX Homo sapiens.

XX WO200194600-A2.

XX 13-DEC-2001.

XX 06-JUN-2001; 2001WO-US018343.

XX 06-JUN-2000; 2000US-0209549P.

XX (GENE-) GENELABS TECHNOLOGIES INC.

XX Kim JP, Starr DB, Tam AW, Laurance ME, Michelotti EP;
 PI Velligan MD, Latour DR, Thomas RL, Kongpachith A, Sheppard LT;
 PI Lim MY, Bruce TW;

XX WPI; 2002-130595/17.

XX New nucleic acid regulatory sequences, which are able to regulate
 PT expression of a gene operably linked to a promoter, useful for regulating
 PT the expression of transgenes and for treating e.g., cancer and
 PT immunological diseases.

XX Claim 13; Page 60; 95pp; English.

PS The invention describes an isolated nucleic acid regulatory sequence for
 XX a cyclin D1 promoter, a CD40L promoter, vancomycin-resistant enterococci
 CC (VRE) promoter, an HBV promoter, androgen receptor (AR) promoter, Human
 CC epidermal growth factor receptor 2 (HER2) promoter, or a beta lactamase
 CC (Bla) promoter. Transcription regulatory sequences may be used to
 CC regulate expression of the endogenous, autologous or heterologous genes
 CC operably linked to the promoter, and may be incorporated into
 CC heterologous nucleic acid constructs for use in regulated expression of
 CC transgenes. Regulated expression of cyclin D1 can be used in cancer
 CC therapies, such as breast, colon or pancreatic cancers and familial
 CC adenomatous polyposis. Regulation of the activity of CD40L gene promoter
 CC may be used in the treatment of immunological disorders, such as
 CC autoimmune diseases e.g. multiple sclerosis (MS), systematic lupus
 CC erythematosus (SLE), graft-vs-host disease (GVHD) and rheumatoid
 CC arthritis. Regulated expression of genes under the control of the HBV
 CC (hepatitis B)-specific core, pre-S and X promoters can be used in the
 CC therapy of HBV disease, chronic hepatic insufficiency, cirrhosis,
 CC hepatocellular carcinoma, and in the regulated expression of liver cell-
 CC specific genes. Regulated expression of the vanH gene promoter can be
 CC used in treatment of Enterococcus infection, while regulated expression
 CC of the androgen receptor gene can be used in the treatment of prostate
 CC cancer. This sequence represents a primer used in the invention to
 CC determine the functions of regions within the selected promoters,
 CC described in the method of the invention

XX Sequence 16 BP; 2 A; 9 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 14.5%; Score 11.2; DB 1; Length 16;

Best Local Similarity 81.2%; Pred. No. 1.2e+02;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 38 CTGAGAGGTAAAGAGC 53

Db 16 CTGGAGGTGGAGAGC 1

RESULT 150

AAL56970/c

ID AAL56970 standard; DNA; 16 BP.

XX AAL56970;

XX 11-MAR-2004 (first entry)

XX Human hypoxia-inducible factor-1 alpha antisense oligo #66.

XX HIF-1alpha; hypoxia-inducible factor-1 alpha; human; antisense; cancer;
 KW pre-eclampsia; cytostatic; gynaecological; antiinflammatory; neurotropic;
 KW neuroprotective; ss.

XX Homo sapiens.

XX WO2003085110-A2.

XX 16-OCT-2003.

XX 04-APR-2003; 2003WO-IB001758.

XX 05-APR-2002; 2002US-0370126P.

XX (CURE-) CUREON AS.

XX Thru CA, Hog AM, Kristjansen PEG;

XX WPI; 2003-812728/76.

XX New oligonucleotide that modulates hypoxia-inducible factor-1alpha,
 PT useful for treating e.g. cancer or Alzheimer's disease.
 XX
 PS Claim 1; Page 42; Opp; English.
 XX
 CC The present invention relates to compounds capable of modulating hypoxia-
 CC inducible factor-1alpha (HIF1a). The compounds are used to treat patients
 CC with, or at risk of developing, cancer (e.g. of breast, prostate,
 CC pancreas, lung), pre-eclampsia, inflammatory bowel disease or Alzheimer's
 CC disease, for modulating angiogenesis, proliferation of erythrocytes and
 CC other cells, iron, glucose and energy metabolism, pH regulation, tissue
 CC invasion, apoptosis, multiple drug resistance, cellular stress responses,
 CC and matrix metabolism, especially apoptosis where modulation is
 CC sensitivity to an apoptotic stimulus, particularly a chemotherapeutic
 CC agent and for inhibiting proliferation of cells (especially cancer cells)
 CC in vitro. The present invention is an antisense oligonucleotide against
 CC HIF1alpha identified in the exemplification of the invention
 XX
 SQ Sequence 16 BP; 0 A; 3 C; 5 G; 8 T; 0 U; 0 Other;
 Query Match 14.5%; Score 11.2; DB 1; Length 16;
 Best Local Similarity 81.2%; Pred. No. 1.2e+02;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 47 AAGAGCCGACGACG 62
 Db 16 AAGACACAGCGACG 1
 RESULT 151
 ABQ86793/C
 ID ABQ86793 standard; cDNA; 11 BP.
 XX
 AC ABQ86793;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Human skin stress/ageing related EST SEQ ID NO 548.
 XX
 KW Human; skin ageing; skin stress; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253773-A2.
 XX
 PD 11-JUL-2002.
 XX
 PP 20-DEC-2001; 2001WO-EP015178.
 XX
 PR 03-JAN-2001; 2001DE-01000121.
 XX
 PA (HENKEL) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-528865/56.
 XX
 PT Identifying genes involved in skin stress and aging, useful e.g. in
 PT screening for cosmetic or therapeutic agents, based on differential gene
 PT expression.
 XX
 PS Claim 8; Page 59; 325pp; German.
 XX
 CC The invention relates to identifying (M1) genes in vitro that, in humans
 CC or animals, are important for skin ageing and/or skin stress by serial
 CC analysis of gene expression between mixtures of transcribed and
 CC optionally translated, genetically encoded factors (A) obtained from
 CC young and aged skin, to identify that genes that show strong differential
 CC expression. (A) comprises protein or mRNAs or their fragments. (M1) is
 CC useful for: identifying markers of skin ageing and/or stress; determining
 CC skin ageing and/or stress; and identifying or determining the effects of
 CC pharmaceutical or cosmetic agents for control of skin ageing. The present

CC sequence is one of a group of human skin ageing/stress related expressed
 CC sequence tags (ABQ86246-ABQ87680) of the invention
 XX
 SQ Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 14.3%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 20 ATACAACCTCTG 30
 Db 11 ATACAACCTCTG 1
 RESULT 152
 ABV71507/C
 ID ABV71507 standard; cDNA; 11 BP.
 XX
 AC ABV71507;
 XX
 DT 21-OCT-2002 (first entry)
 XX
 DE Human skin EST 9293.
 XX
 KW Human; skin; dermatological; vulnery; antipsoriatic; antiseborrheic;
 KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
 KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200253774-A2.
 XX
 PD 11-JUL-2002.
 XX
 PP 20-DEC-2001; 2001WO-EP015179.
 XX
 PR 03-JAN-2001; 2001DE-01000127.
 XX
 PA (HENKEL) HENKEL KGAA.
 XX
 PI Petersohn D, Conradt M, Hofmann K;
 XX
 DR WPI; 2002-590638/63.
 XX
 PT In vitro identification of skin-expressed genes, useful for determining
 PT homeostasis and identifying cosmetic or pharmaceutical agents against
 PT e.g. skin cancer.
 XX
 PS Claim 24; Page 299; 1345pp; German.
 XX
 CC The invention relates to in vitro identification (M1) of genes expressed
 CC in the skin of humans or animals by subjecting a mixture of genetically
 CC encoded factors from skin, to serial analysis of gene expression (SAGE)
 CC so as to identify skin-expressed genes and quantify their expression.
 CC (M1) is useful for identifying genes involved in skin homeostasis; to
 CC determine skin homeostasis and to test agent (A) that maintains or
 CC promotes skin homeostasis or that can be used for treating skin
 CC disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
 CC ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
 CC rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
 CC skin. The present sequence is that of a human expressed sequence tag
 CC (EST) of the invention
 XX
 SQ Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 14.3%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 20 ATACAACCTCTG 30
 Db 11 ATACAACCTCTG 1

```

RESULT 153
ABV64086/c
ID ABV64086 standard; cDNA; 11 BP.
XX
XX
AC ABV64086;
DT 21-OCT-2002 (first entry)
XX
XX Human skin EST 1872.
XX
XX Human; skin; dermatological; vulnery; antipeoriatic; antiseborrhaeic;
KW immunosuppressive; antiinflammatory; cytostatic; SAGE; neurodermatitis;
KW psoriasis; dermatitis; skin cancer; EST; expressed sequence tag; ss.
XX
XX Homo sapiens.
XX
XX WO200253774-A2.
XX
XX 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-EP015179.
XX
XX 03-JAN-2001; 2001DE-01000127.
XX (HENKEL KGAA.
XX
XX Petersohn D, Conradt M, Hofmann K;
XX
XX WPI; 2002-590638/63.
XX
XX In vitro identification of skin-expressed genes, useful for determining
XX homeostasis and identifying cosmetic or pharmaceutical agents against
XX e.g. skin cancer.
XX
XX Disclosure; Page 76; 1345pp; German.
XX
XX The invention relates to in vitro identification (MI) of genes expressed
XX in the skin of humans or animals by subjecting a mixture of genetically
XX encoded factors from skin, to serial analysis of gene expression (SAGE)
XX so as to identify skin-expressed genes and quantify their expression.
XX (MI) is useful for identifying genes involved in skin homeostasis; to
XX determine skin homeostasis and to test agent (A) that maintains or
XX promotes skin homeostasis or that can be used for treating skin
XX disorders, specifically neurodermatitis; sunburn; psoriasis; scleroderma;
XX ichthyosis; atopic dermatitis; acne; seborrhea; lupus erythematosus;
XX rosacea; melanoma; basal cell carcinoma; and carcinoma or sarcoma of the
XX skin. The present sequence is that of a human expressed sequence tag
XX (EST) of the invention
XX
XX Sequence 11 BP; 3 A; 1 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATACAACTCTG 30
DB 11 ATACAACTCTG 1
|||||

RESULT 154
ACCS8751
ID ACC58751 standard; DNA; 11 BP.
XX
XX ACC58751;
XX
XX 26-AUG-2003 (first entry)
XX
XX Anti-restenosis phosphorothioate oligonucleotide hairpin loop region.
DE Anti-restenosis phosphorothioate oligonucleotide hairpin loop region.
XX
XX Anti-restenosis; vasotropic; phosphorothioate; ss.
XX

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OS Synthetic.
XX
XX Key Location/Qualifiers
FH stem_loop 1..11
FT /*tag= a
FT modified_base 1..11
FT /*tag= b
FT /mod_base= OTHER
FT /note= "OTHER= phosphorothioate nucleotides"
XX
XX WO2003035666-A2.
XX
XX 01-MAY-2003.
XX
XX 25-OCT-2002; 2002WO-EP011964.
XX
XX 26-OCT-2001; 2001GB-00025746.
XX
XX (CATH-) CATHNET-SCI HOLDING AS.
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Andersen E, Le Doan T, Lamidey L;
XX
XX WPI; 2003-504990/47.
XX
XX Anti-restenosis agent for treating restenosis e.g. in smooth muscle
XX tissue, comprises a phosphorothioate-modified oligonucleotide comprising
XX one hairpin loop and a dt or dg releasing group.
XX
XX Claim 5; Page 32; 39pp; English.
XX
XX The present sequence comprises the 5' or (preferably) 3' terminal hairpin
XX loop region of anti-restenosis phosphorothioate oligonucleotides of the
XX invention (see also ACC58756-57). A claimed oligonucleotide for treating
XX restenosis, e.g. in smooth muscle tissue, comprises a phosphorothioate
XX modified oligonucleotide that includes at least one hairpin loop, a dt or
XX dg releasing group and at least one multi-guanosine sequence. The
XX oligonucleotide has a long active life in vivo due to the presence of the
XX hairpin loop. It may be used as, or in, a coating on a device for
XX implantation into the body, e.g. a stent for use in percutaneous
XX transluminal coronary angioplasty (PTCA)
XX
XX Sequence 11 BP; 3 A; 3 C; 4 G; 1 T; 0 U; 0 Other;
SQ
Query Match 14.3%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTG 64
DB 1 CAGCGAAGCTG 11
|||||

RESULT 155
AAQ24027/c
ID AAQ24027 standard; DNA; 12 BP.
XX
XX AAQ24027;
XX
XX 25-MAR-2003 (revised)
DT 21-SEP-1992 (first entry)
XX
XX Herpesvirus inhibiting antisense oligonucleotide.
DE
XX HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;
KW Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.
XX
XX Synthetic.
XX
XX WO9205284-A.
XX
XX 02-APR-1992.
XX

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PP 18-SEP-1991; 91WO-US006646.
XX
PR 21-SEP-1990; 90US-00586185.
XX
PA (UTMA-) UNIV MARYLAND BALTIMORE.
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Aurelian L, Tso P;
XX
XX WPI; 1992-132145/16.
XX
XX New anti-sense oligo:nucleotide(s) for inhibiting HSV - also used for
XX diagnosis and for inhibiting HIV activation by herpes virus.
XX
XX Claim 1; Page 38; 77pp; English.
XX
XX The sequence is that of an antisense oligonucleotide which can be used
XX for inhibiting growth or replication of herpesviruses. It corresponds to
XX an antisense sequence of a herpesvirus site, pref. in a gene that is
XX essential for synthesising nucleic acids e.g. the immediate early genes
XX or Vmw65. It can be prepd. by solid phase triester or phosphor- amidite
XX chemistry or by recombinant DNA techniques. It can be used for treating
XX infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2
XX (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus
XX (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the
XX inhibition of herpesvirus growth or replication may indirectly forestall
XX the progression of events from HIV exposure to the clinical manifestation
XX of AIDS. It may also be useful in the detection, diagnosis and
XX manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-
XX Q24044. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 12 BP; 4 A; 3 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCT 39
Db 11 TGGAGTCCTCT 1

RESULT 156
ABI20955/c
ID ABI20955 standard; DNA; 12 BP.
XX
AC ABI20955;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide primer SEQ ID NO 320928 for detecting SNP TSC0029975.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 14594; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
XX Claim 1; SEQ ID NO 320928; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 12 BP; 1 A; 6 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GAGAGGTAAG 50
Db 12 GAGAGGTAAG 2

RESULT 157
ABC14587/c
ID ABC14587 standard; DNA; 13 BP.
XX
AC ABC14587;
XX
XX 20-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 14594 for detecting SNP TSC0003290.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 14594; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX

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CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 1 Other;
 Query Match 14.3%; Score 11; DB 1; Length 13;
 Best Local Similarity 84.6%; Pred. No. 1e+02;
 Matches 11; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 41 AGAGGTAAGCAGC 53
 DB 13 AGAAGTAAGAGY 1

RESULT 158
 ABF82001/c
 ID ABF82001 standard; DNA; 13 BP.

XX AC ABF82001;

XX 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 181998 for detecting SNP TSC0044987.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 181998; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 3 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAA 49
 |||||

Db 12 TGAGAGGTAAA 2

RESULT 159

ABF82000
 ID ABF82000 standard; DNA; 13 BP.

XX AC ABF82000;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 181997 for detecting SNP TSC0044987.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.

XX 07-APR-2000; 2000DE-01019173.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

XX Claim 1; SEQ ID NO 181997; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 13 BP; 6 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAA 49
 |||||

Db 2 TGAGAGGTAAA 12

RESULT 160

ABH24941/c
 ID ABH24941 standard; DNA; 13 BP.

XX AC ABH24941;

XX 22-FEB-2002 (first entry)

XX Oligonucleotide SEQ ID NO 224918 for detecting SNP TSC0054826.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 13 BP; 8 A; 0 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 14.3%; Score 11; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTAAGA 51
 Db 2 AGAGGTAAGA 12
 |||||

RESULT 163
 AAA26129
 ID AAA26129 standard; DNA; 14 BP.

XX
 AC AAA26129;

XX 19-JUL-2000 (first entry)

XX Oestrogen receptor hairpin ribozyme target sequence SEQ ID NO:2627.

XX Oestrogen receptor; c-ras; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.

XX Homo sapiens.

XX WO9954459-A2.

XX 28-OCT-1999.

XX 19-APR-1999; 99WO-US008547.

XX 20-APR-1998; 98US-0082404P.

XX 23-JUN-1998; 98US-00103636.

XX (RIBO-) RIBOZYME PHARM INC.

XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;

XX WPI; 2000-013248/01.

XX New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.

XX Claim 79; Page 99; 148pp; English.

XX The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodi(thio)ate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research

CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention

XX
 SQ Sequence 14 BP; 2 A; 4 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 14.3%; Score 11; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 ACGGCTCTGGG 19
 Db 3 ACGGCTCTGGG 13
 |||||

RESULT 164
 ABT13117
 ID ABT13117 standard; DNA; 14 BP.

XX
 AC ABT13117;

XX 30-JAN-2003 (first entry)

XX Fanconi anaemia FANCD intron/exon junction oligo SEQ ID NO 20.

XX Cytostatic; dermatological; vasotropic; anti-anaemic; FA pathway defect;
 KW Fanconi anaemia protein complex; FANCD; DNA repair; Cockayne's syndrome;
 KW cell cycle abnormality; Fanconi anaemia; ataxia telangiectasia; cancer;
 KW Bloom's syndrome; Hereditary non-polyposis colon cancer; gene therapy;
 KW Xeroderma pigmentosum; ds.

XX Unidentified.

XX WO200236761-A2.

XX 10-MAY-2002.

XX 02-NOV-2001; 2001WO-US045561.

XX 03-NOV-2000; 2000US-0245756P.

XX (DAND) DANA FARBER CANCER INST INC.

XX D'andrea AD, Taniguchi T, Timmers C, Grompe M;

XX WPI; 2002-519251/55.

XX Novel isolated Fanconi anemia protein complex polypeptide, termed FANCD2,
 PT useful for treating Fanconi anemia pathway defect in cell target or for
 PT treating patient with defective FANCD2 gene.

XX Claim 7; Page 54; 103pp; English.

XX The invention relates to an isolated Fanconi anaemia protein complex
 CC (FANCD2) polypeptide. The FANCD2 protein comprises a sequence of 1472
 CC amino acids fully defined in the specification, its 90% identical
 CC sequence, a sequence encoded by a polynucleotide that is at least 90%
 CC identical to sequences given in specification such as a 5127 base pair
 CC sequence, or a fragment which is at least 50 amino acids in length. The
 CC FANCD2 protein is useful for treating a FA pathway defect in a cell
 CC target or for treating a patient with a defective FANCD2 gene. The FANCD2
 CC gene is useful for making a recombinant expression vector. The FANCD2
 CC protein and its gene are useful as a novel target for therapeutic
 CC development, and in diagnostic test and screening assays for diseases
 CC associated with DNA repair and cell cycle abnormalities such as Fanconi
 CC anaemia, Bloom's syndrome, Cockayne's syndrome, Hereditary non-polyposis

CC angioplastic restenosis. By inhibiting CETP, the levels of HDL and low
 CC density lipoproteins (LDL), and the HDL:LDL ratio are favourably altered
 CC (a decrease in LDL levels, and a corresponding increase in HDL levels).
 CC The HH ribozymes can also be used diagnostically to study genetic drift
 CC and mutations in diseased cells, and to detect CETP mRNA. As the HH
 CC ribozymes target specific regions of the CETP gene, they have low non-
 CC specific activity
 XX
 SQ Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;
 Query Match 14.3%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 GTCCTCTGAGA 43
 DB 15 GTCCTCTGAGA 5
 |||||
 RESULT 167
 AAZ64343/c
 ID AAZ64343 standard; RNA; 15 BP.
 XX
 AC AAZ64343;
 XX
 DT 28-MAR-2000 (first entry)
 XX
 DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 8121.
 XX
 KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO9955847-A2.
 XX
 PD 04-NOV-1999.
 XX
 PF 26-APR-1999; 99WO-US009027.
 XX
 PR 27-APR-1998; 98US-0083217P.
 PR 18-SEP-1998; 98US-0100842P.
 PR 25-FEB-1999; 99US-00257608.
 PR 23-MAR-1999; 99US-00274553.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
 XX
 DR WPI; 2000-062023/05.
 XX
 PT Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection.
 XX
 PS Claim 1; Page 89; 123pp; English.
 XX
 CC The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer
 XX

SQ Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other;
 Query Match 14.3%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 45 GTAAAGAGCCA 55
 DB 13 GTAAAGAGCCA 3
 |||||
 RESULT 168
 AAZ64344/c
 ID AAZ64344 standard; RNA; 15 BP.
 XX
 AC AAZ64344;
 XX
 DT 28-MAR-2000 (first entry)
 XX
 DE Substrate for hammerhead ribozyme which cleaves HCV RNA at nt. 8123.
 XX
 KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO9955847-A2.
 XX
 PD 04-NOV-1999.
 XX
 PF 26-APR-1999; 99WO-US009027.
 XX
 PR 27-APR-1998; 98US-0083217P.
 PR 18-SEP-1998; 98US-0100842P.
 PR 25-FEB-1999; 99US-00257608.
 PR 23-MAR-1999; 99US-00274553.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
 XX
 DR WPI; 2000-062023/05.
 XX
 PT Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection.
 XX
 PS Claim 1; Page 89; 123pp; English.
 XX
 CC The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
 CC the descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
 Query Match 14.3%; Score 11; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 45 GTAAAGAGCCA 55
 |||||

CC colon cancer, ataxia telangiectasia and Xeroderma pigmentosum. The FANCD2
 CC gene is useful in producing probes and primers for screening patients in
 CC genetic based test, for diagnosing Fanconi anaemia and cancer, for
 CC preparing an experimental mouse model for use in screening new
 CC therapeutics for treating conditions involving defective DNA repair, and
 CC in gene therapy methods. A recombinant vector containing the FANCD2 gene
 CC of the invention is useful in gene therapy. This polynucleotide sequence
 CC represents a FANCD intron/exon junction oligonucleotide relating to the
 CC invention

XX Sequence 14 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 14.3%; Score 11; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 43 AGGTAAAGAGC 53
 Db 2 AGGTAAAGAGC 12
 |||||

RESULT 165
 ADC42354
 ID ADC42354 standard; DNA; 14 BP.
 XX AC
 AC ADC42354;
 AC
 DT 18-DEC-2003 (first entry)
 XX
 DE Human FANCD exon 12 5'-donor site SEQ ID NO:19.
 XX
 KW human; cancer; Fanconi Anaemia; FA; BRCA; cytostatic; microarray;
 KW chemosensitising; da.
 KW
 OS Homo sapiens.
 XX
 XX WO2003039327-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 06-JUN-2002; 2002WO-US018153.
 XX
 PR 02-NOV-2001; 2001US-00998027.
 PR
 PR 02-NOV-2001; 2001WO-US045561.
 XX
 XX (DAND) DANA FARBER CANCER INST.
 PA (UFOR-) UNIV OREGON HEALTH SCI.
 XX
 XX D'andrea AD, Taniguchi T, Timmers C, Grompe M, Fox EA;
 PI
 XX WPI; 2003-441436/41.
 DR
 XX
 XX Diagnosing or determining cancer or increased risk of cancer in a
 PT patient, by testing Fanconi Anemia/BRCA pathway gene or protein for a
 PT cancer-associated defect, that indicates cancer or increased risk of
 PT cancer.

XX
 XX Example 4; SEQ ID NO 20; 160pp; English.

XX The invention relates to a novel method of diagnosing or determining if a
 CC patient has cancer or is at increased risk of cancer, involving testing a
 CC Fanconi Anaemia (FA)/BRCA pathway gene or protein for the presence of a
 CC cancer-associated defect, where the presence of one or more cancer-
 CC associated defects is indicative of cancer or an increased risk of cancer
 CC in the patient. The method of the invention has cytostatic activity. The
 CC method is useful for determining if a patient has cancer, or is at
 CC increased risk of developing cancer, e.g. breast, ovarian or prostate
 CC cancer. A microarray of the invention is useful for determining if a
 CC patient has cancer, or is at increased risk of developing cancer, by
 CC hybridising a nucleic acid sample to the nucleic acid sequences from the
 CC array, and detecting the presence of mutations in FA/BRCA pathway genes
 CC in the nucleic acid sample from the patient, where detecting the presence
 CC of mutations is indicative of a patient who has cancer, or is at

CC increased risk of developing cancer. A method of the invention is useful
 CC for screening a chemosensitising agent, and the agent obtained is useful
 CC for treating a patient having a cancer. The present sequence is used in
 CC the exemplification of the invention.

XX Sequence 14 BP; 6 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 14.3%; Score 11; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 43 AGGTAAAGAGC 53
 Db 2 AGGTAAAGAGC 12
 |||||

RESULT 166
 AAT49756/C
 ID AAT49756 standard; RNA; 15 BP.
 XX AC
 AC AAT49756;
 AC
 DT 02-MAR-1997 (first entry)
 XX
 DE Human CERP HH ribozyme target sequence #906.
 XX
 KW Hammerhead ribozyme; cholesterol ester transfer protein; mRNA cleavage;
 KW neutral lipid transfer; plasma lipoprotein; atherosclerosis; atherectomy;
 KW reverse cholesterol transport; high density lipoprotein; therapy; CERP;
 KW familial hypercholesterolaemia; dyslipidaemia; hypoalphalipoproteinaemia;
 KW peripheral vascular disease; hyperbetalipoproteinaemia; RCT; inhibitor;
 KW angioplastic restenosis; low density lipoprotein; diabetes; HDL; human;
 KW LDL; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9620279-A1.
 XX
 PD 04-JUL-1996.
 XX
 PF 11-DEC-1995; 95WO-US016000.
 XX
 PR 23-DEC-1994; 94US-00363240.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (WARN) WARNER LAMBERT CO.
 XX
 XX Couture L, Stinchcomb D, Mcswiggen J, Bisgaier C, Pape M;
 XX WPI; 1996-321852/32.
 XX
 XX New ribozyme(s) for cleaving cholesterol ester transfer protein mRNA -
 PT useful for preventing or treating initial development, progression or
 PT regression of vascular diseases, esp. familial hypercholesterolaemia.
 XX
 PS Claim 4; Page 31; 72pp; English.

XX AAT49608-T49863 represent target sequences for the human cholesterol
 CC ester transfer protein (CERP) hammerhead (HH) ribozymes (see AAT49881-
 CC T50137). CERP is a 74 kD glycoprotein that facilitates neutral lipid
 CC transfer between plasma lipoproteins. The numbering of the targets refers
 CC to the position of the cleavage site in full length CERP. The ribozyme
 CC binds to 5 nucleotides either side of this site, provided the sequence
 CC is immediately upstream. The ribozymes are able to cleave mRNA from the
 CC gene encoding CERP, thereby blocking synthesis and/or expression of the
 CC mRNA. By inhibiting CERP, the reverse cholesterol transport (RCT) pathway
 CC can be inhibited (or eliminated) thereby preventing the reduction in size
 CC density of the high density lipoproteins (HDL), prolonging HDL half life,
 CC and therefore increasing HDL levels. The ribozymes can be used to treat
 CC conditions associated with abnormal levels of CERP, specifically familial
 CC hypercholesterolaemia, atherosclerosis, peripheral vascular disease,
 CC hyperbetalipoproteinaemia, hypoalphalipoproteinaemia, dyslipidaemia,
 CC vascular complications of diabetes, transplant, atherectomy and

Db 11 GTRAGGCCA 1

RESULT 169
AAD25954
ID AAD25954 standard; DNA; 15 BP.
AC AAD25954;
XX
XX 26-MAR-2002 (first entry)
XX
XX ASO probe #7 to detect human P14 gene polymorphisms.
XX
XX Human; protease inhibitor; P14; kallistatin; therapy; polymorphic site;
KW PS; haplotyping; genotyping; acute pancreatitis; drug screening;
KW antiinflammatory; chromosome 14q31-q32.1; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200179227-A2.
XX
XX 25-OCT-2001.
XX
XX 13-APR-2001; 2001WO-US012255.
XX
XX 13-APR-2000; 2000US-0196990P.
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Choi JY, Koshiy B, Sanchis A;
XX WPI; 2002-075060/10.
XX
XX Genotyping protease inhibitor 4 gene of individual for determining
PT haplotype of individual, involves determining identity of nucleotide pair
PT at specific polymorphic sites for two copies of gene.
XX
XX Claim 16; Page 13; 79pp; English.
XX
XX The present invention relates to genotyping protease inhibitor (PI) 4
CC (kallistatin) gene of an individual, involves determining for the two
CC copies of the P14 gene present in the individual, the identity of the
CC nucleotide pair at one or more polymorphic sites. P14 gene is located on
CC chromosome 14q31-q32.1. Genotyping is useful for determining if an
CC individual has a haplotype or haplotype pairs defined in the
CC specification. Haplotyping is useful for improving the efficacy and
CC reliability of several steps in the discovery and development of drugs
CC for treating diseases associated with P14 activity, e.g. acute
CC pancreatitis, to validate P14 as a candidate agent for treating a
CC specific condition or disease predicted to be associated with P14
CC activity, and in the design of clinical trials of candidate drugs for
CC treating a specific condition or disease predicted to be associated with
CC P14 activity. The P14 gene is useful in studying the expression and
CC function of P14, and in expressing P14 protein for use in screening for
CC candidate drugs to treat diseases related to P14 activity. The present
CC sequence is a ASO (allele-specific oligonucleotide) probe to detect human
XX P14 gene polymorphisms
XX
SQ Sequence 15 BP; 2 A; 4 C; 4 G; 4 T; 0 U; 1 Other;
Query Match 14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 61 GCTGATGCTCTGT 73
|||:|||||
3 GCAGAGTCTCTGT 15

Db 3 GCAGAGTCTCTGT 15

RESULT 170
ABL88306/C
ID ABL88306 standard; DNA; 15 BP.
XX

AC ABL88306;
XX
XX 20-MAY-2002 (first entry)
XX
XX Human CHRNA allele-specific oligonucleotide (ASO) primer, SEQ ID NO:40.
XX
XX Human; cholinergic receptor nicotinic epsilon polypeptide; CHRNA;
KW chromosome 17p13-12; acetylcholine receptor; AChR;
KW neuromuscular junction; skeletal muscle; postnatal development;
KW congenital myasthenic syndrome; CMS; haplotyping; genotyping; haplotype;
KW genetic variant; single nucleotide polymorphism; SNP; gene therapy;
KW drug screening; allele-specific oligonucleotide; ASO; primer; ss.
XX
XX Homo sapiens.
OS
XX WO200198316-A2.
XX
XX 27-DEC-2001.
XX
XX 20-JUN-2001; 2001WO-US019835.
XX
XX 20-JUN-2000; 2000US-0212870P.
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Amaro E, Bieganski KM, Klem SE, Koshiy B, Tanguay DA;
XX WPI; 2002-130787/17.
XX
XX Novel genetic variants of cholinergic receptor, nicotinic, epsilon
PT polypeptide gene useful in studying expression and function of the
PT protein, and for screening drugs to treat diseases e.g. congenital
PT myasthenic syndrome.
XX
XX Claim 17; Page 14; 104pp; English.
XX
XX The invention relates to a method for haplotyping the cholinergic
CC receptor, nicotinic, epsilon polypeptide (CHRNA) gene (ABL88268) of an
CC individual, and also describes 17 novel polymorphic sites within the
CC human CHRNA gene. The CHRNA gene is located on chromosome 17p13-12 and
CC contains 12 exons which encode a 493 amino acid protein (AB49112). The
CC CHRNA protein is one of the 5 subunits of mammalian acetylcholine
CC receptors (AChRs) found at neuromuscular junctions in juveniles and
CC adults, and is essential for the normal postnatal development of skeletal
CC muscle. Mutations in the CHRNA gene are associated with congenital
CC myasthenic syndrome (CMS). CHRNA gene sequences can therefore be used in
CC gene therapy. The CHRNA gene is also useful for studying the expression
CC and function of CHRNA, and in expressing CHRNA protein for use in
CC screening for candidate drugs to treat diseases related to CHRNA. The
CC method of the invention is useful for haplotyping the CHRNA gene in an
CC individual, and can also be used in pharmaceutical research to validate
CC CHRNA as a candidate target for, and in design of clinical trials of
CC candidate drugs for, treating a specific condition or disease
CC predicted to be associated with CHRNA activity such as CMS. Polymorphisms
CC in the target region may be determined by the use of allele-specific
CC oligonucleotides (ASOs; ABL88370-ABL88320) as probes and primers, and by
CC primer extension using oligonucleotide primers comprising sequences
CC ABL88371-ABL88354. The CHRNA protein is useful for improving the
CC efficiency and reliability of several steps in the discovery and
CC development of drugs for treating diseases associated with CHRNA
CC activity, and may be used to screen drugs which target CHRNA. Sequences
CC ABL88287-ABL88320 represent specifically claimed allele-specific
CC oligonucleotide (ASO) primers used for detecting polymorphisms in the
XX CHRNA gene
XX
SQ Sequence 15 BP; 3 A; 6 C; 2 G; 3 T; 0 U; 1 Other;
Query Match 14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 84.6%; Pred. No. 1.2e+02;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 33 GTCCTCTGAGAGG 45
:|:|||||

```

Db      14 KTACTCTGAGAGG 2
RESULT 171
ABX01396/c
ID      ABE01396 standard; RNA; 15 BP.
XX
AC      ABE01396;
XX
AC      ABE01396;
XX
DT      23-DEC-2002 (first entry)
XX
DE      Hepatitis C virus substrate #1178 for HCV hammerhead ribozyme #1178.
XX
KW      Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW      HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW      liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW      type I interferon; interferon alpha; interferon beta; cytostatic;
KW      interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW      substrate; hammerhead ribozyme; HH ribozyme; ss.
XX
OS      Hepatitis C virus.
XX
PN      US2002082225-A1.
XX
PD      27-JUN-2002.
XX
PF      23-MAR-1999; 99US-00274553.
XX
PR      23-MAR-1999; 99US-00274553.
XX
PA      (BLAT/) BLATT L.
PA      (MCSW/) MCSWIGGEN J A.
PA      (ROBE/) ROBERTS B.
PA      (PAVC/) PAVCO P A.
PA      (MACE/) MACEJACK D.
XX
PI      Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
XX
DR      WPI; 2002-617759/66.
XX
PT      New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT      replication and are useful to treat hepatitis C virus infections and
PT      cirrhosis, liver failure or hepatocellular carcinoma.
XX
PS      Claim 1; Page 55; 80pp; English.
XX
CC      The present invention relates to enzymatic nucleic acids which
CC      specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC      enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC      (HP) motif where the binding arms comprise sequences complementary to one
CC      of the substrate sequences defined in the specification. The HCV
CC      ribozymes are useful for modulating the expression and/or replication of
CC      hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC      HCV. They can be used to treat cirrhosis, liver failure and/or
CC      a condition associated with HCV infection in conjunction with one or more
CC      other drug therapies, particularly type I interferon, especially
CC      interferon alpha, beta or gamma or consensus interferon. The present
CC      sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC      Some of the sequence data for this patent did not form part of the
CC      printed specification. The complete sequence data for this patent was
CC      obtained in electronic format directly from the USPTO web site at
CC      seqdata.uspto.gov/psipdIDEntry.html
XX
SQ      Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other;

Query Match      14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 GTAAAGAGCCA 55
        |||||
Db      13 GTAAAGAGCCA 3

RESULT 173

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AEB76104/C
ID AEB76104 standard; RNA; 15 BP.
XX AC AEB76104;
XX DT 22-SEP-2005 (first entry)
XX DE Hepatitis C virus hammerhead ribozyme substrate sequence.
XX KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
XX KW antiviral; gene therapy; substrate; ss.
XX OS Hepatitis C virus.
XX PN US2002013458-A1.
XX PD 31-JAN-2002.
XX PP 15-FEB-2000; 2000US-00504231.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLATT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS E.
XX PA (PAVO/) PAVO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX WP; 2002-215899/27.
XX PT New enzymatic nucleic acid molecule, which specifically cleaves minus
XX strand RNA derived from hepatitis C virus, useful for modulating the
XX expression and/or replication of hepatitis C virus.
XX PS Example 1; Page 40; 65pp; English.
XX CC The invention relates to an enzymatic nucleic acid molecule which
XX specifically cleaves minus strand RNA derived from hepatitis C virus
XX (HCV). The binding arms of the molecule comprise ribozyme sequences. The
XX molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
XX Zinzyme motifs. Also described: (1) a pharmaceutical composition
XX comprising the novel enzymatic nucleic acid; (2) a mammalian cell
XX comprising a nucleic acid sequence encoding at least one enzymatic
XX nucleic acid molecule, in a manner, which allows expression of that
XX molecule; (4) a mammalian cell including an expression vector of (3); (5)
XX methods for treating cirrhosis, liver failure or hepatocellular carcinoma
XX by administering to a patient the novel enzymatic nucleic acid or the
XX associated with HCV infection, by contacting cells of the patient with
XX the nucleic acid molecule, and further employing one or more drug
XX therapies; (7) a method for inhibiting HCV replication in a mammalian
XX cell by administering the novel enzymatic nucleic acid; and (8) a method
XX of cleaving a separate RNA molecule by contacting the novel enzymatic
XX nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
XX is useful for modulating the expression and/or replication of hepatitis C
XX virus (HCV), and for inhibiting the expression of HCV minus strand. The
XX nucleic acid may also be used to treat or prevent the occurrence of a
XX disease state in a patient. The present sequence represents an HCV
XX hammerhead ribozyme target substrate sequence which is used in the
XX exemplification of the present invention.
XX SQ Sequence 15 BP; 4 A; 3 C; 3 G; 0 T; 5 U; 0 Other;
Query Match 14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 45 GTAAAGGCCA 55
Db 13 GTAAAGGCCA 3

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RESULT 174
AEB76105/C
ID AEB76105 standard; RNA; 15 BP.
XX AC AEB76105;
XX DT 22-SEP-2005 (first entry)
XX DE Hepatitis C virus hammerhead ribozyme substrate sequence.
XX KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
XX KW antiviral; gene therapy; substrate; ss.
XX OS Hepatitis C virus.
XX PN US2002013458-A1.
XX PD 31-JAN-2002.
XX PP 15-FEB-2000; 2000US-00504231.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLATT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS E.
XX PA (PAVO/) PAVO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX WP; 2002-215899/27.
XX PT New enzymatic nucleic acid molecule, which specifically cleaves minus
XX strand RNA derived from hepatitis C virus, useful for modulating the
XX expression and/or replication of hepatitis C virus.
XX PS Example 1; Page 40; 65pp; English.
XX CC The invention relates to an enzymatic nucleic acid molecule which
XX specifically cleaves minus strand RNA derived from hepatitis C virus
XX (HCV). The binding arms of the molecule comprise ribozyme sequences. The
XX molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
XX Zinzyme motifs. Also described: (1) a pharmaceutical composition
XX comprising the novel enzymatic nucleic acid; (2) a mammalian cell
XX comprising a nucleic acid sequence encoding at least one enzymatic
XX nucleic acid molecule, in a manner, which allows expression of that
XX molecule; (4) a mammalian cell including an expression vector of (3); (5)
XX methods for treating cirrhosis, liver failure or hepatocellular carcinoma
XX by administering to a patient the novel enzymatic nucleic acid or the
XX associated with HCV infection, by contacting cells of the patient with
XX the nucleic acid molecule, and further employing one or more drug
XX therapies; (7) a method for inhibiting HCV replication in a mammalian
XX cell by administering the novel enzymatic nucleic acid; and (8) a method
XX of cleaving a separate RNA molecule by contacting the novel enzymatic
XX nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
XX is useful for modulating the expression and/or replication of hepatitis C
XX virus (HCV), and for inhibiting the expression of HCV minus strand. The
XX nucleic acid may also be used to treat or prevent the occurrence of a
XX disease state in a patient. The present sequence represents an HCV
XX hammerhead ribozyme target substrate sequence which is used in the
XX exemplification of the present invention.
XX SQ Sequence 15 BP; 2 A; 4 C; 4 G; 0 T; 5 U; 0 Other;
Query Match 14.3%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314397.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.
 PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 PA (RIBO-) RIBOZYME PHARM INC.
 PI Stinchcomb DT, Chowira B, Dizenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FR, Woolf T;
 XX WPI; 1995-351090/45.
 DR Ribozyms having modified bases and methods for producing them - for use
 XX in inhibiting disease related genes.
 XX Claim 2; Page 220; 407pp; English.
 CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves interleukin-5 (IL-
 CC 5) mRNA at the nucleotide base position indicated in the DE line. Regions
 CC of the mRNA that do not form secondary folding structures and that
 CC contain potential hammerhead and hairpin ribozyme cleavage sites were
 CC identified by computer analysis. Ribozymes directed against these mRNA
 CC sequences were designed and synthesised with modifications that improve
 CC their nuclease resistance. The ribozymes cleave the IL-5 target sequences
 CC and thereby inhibit IL-5 expression, making them useful for treating
 CC chronic asthma, e.g. by inhibiting the synthesis of IL-5 in lymphocytes
 CC and preventing the recruitment and activation of eosinophils. The
 CC ribozymes can also be used to treat eosinophilia (related to parasitic
 CC infection or with pulmonary infiltration) and L-tryptophan-associated
 CC eosinophilia-myalgia syndrome. (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX SQ Sequence 15 BP; 5 A; 3 C; 4 G; 0 T; 3 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 25 ACTCTGGAGTCCTC 38
 Db ||||| |||||
 14 ACTCTGAAGTCCTC 1
 RESULT 177
 AAT55140
 ID AAT55140 standard; RNA; 15 BP.
 XX
 AC AAT55140;
 AC
 DT 25-MAR-2003 (revised)
 DT 21-APR-1997 (first entry)
 XX Human relA hammerhead ribozyme target sequence (nt. position 1566).
 DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 XX Gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW

KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 XX 88.
 OS Homo sapiens.
 XX W09523225-A2.
 XX 31-AUG-1995.
 XX 23-FEB-1995; 95WO-IB000156.
 XX 23-FEB-1994; 94US-00201109.
 XX 29-MAR-1994; 94US-00218934.
 XX 04-APR-1994; 94US-00222795.
 XX 07-APR-1994; 94US-00224483.
 XX 15-APR-1994; 94US-00227958.
 XX 15-APR-1994; 94US-00228041.
 XX 18-MAY-1994; 94US-00245736.
 XX 06-JUL-1994; 94US-00271280.
 XX 15-AUG-1994; 94US-00291932.
 XX 16-AUG-1994; 94US-00291433.
 XX 17-AUG-1994; 94US-00292620.
 XX 19-AUG-1994; 94US-00293520.
 XX 02-SEP-1994; 94US-00300000.
 XX 08-SEP-1994; 94US-00303039.
 XX 23-SEP-1994; 94US-00311486.
 XX 23-SEP-1994; 94US-00311749.
 XX 28-SEP-1994; 94US-00314397.
 XX 03-OCT-1994; 94US-00316771.
 XX 07-OCT-1994; 94US-00319492.
 XX 11-OCT-1994; 94US-00321993.
 XX 04-NOV-1994; 94US-00334847.
 XX 10-NOV-1994; 94US-00337608.
 XX 28-NOV-1994; 94US-00345516.
 XX 16-DEC-1994; 94US-00357577.
 XX 23-DEC-1994; 94US-00363233.
 XX 30-JAN-1995; 95US-00380734.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Stinchcomb DT, Chowira B, Dizenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Usman N, Wincott FR, Woolf T;
 XX WPI; 1995-351090/45.
 DR Ribozyms having modified bases and methods for producing them - for use
 XX in inhibiting disease related genes.
 XX Claim 2; Page 229; 407pp; English.
 CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the
 CC nucleotide base position indicated in the DE line. The relA gene product
 CC is a subunit of the transcriptional regulator NF-kappaB and is implicated
 CC specifically in the induction of inflammatory responses. Regions of the
 CC mRNA that do not form secondary folding structures and that contain
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified
 CC by computer analysis. Ribozymes directed against these mRNA sequences
 CC were designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit relA expression, making them potentially
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well
 CC as for increasing tolerance to transplanted tissues. The potential
 CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means
 CC that uses are limited to local delivery, acute indications or ex vivo
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
 XX

```
SQ Sequence 15 BP; 4 A; 3 C; 5 G; 0 T; 3 U; 0 Other;
Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 1.3e+02;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTGAG 42
      |||||: |||||
Db 2 UGGAGUACCCUGAG 15

RESULT 178
AAZ62575/c
ID AAZ62575 standard; RNA; 15 BP.
AC AAZ62575;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for HH ribozyme HCV-3329 which cleaves HCV RNA at nt. 3329.
XX
DE Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
PN W09955847-A2.
XX
PI 04-NOV-1999.
XX
PF 26-APR-1999; 99WO-US009027.
XX
PR 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
XX
PT Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
XX
PS Claim 1; Page 56; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 15 BP; 3 A; 3 C; 5 G; 0 T; 4 U; 0 Other;
Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGTCC 70
      ||||| |||||
```

```
Db 15 CCAAGATGATGTCC 2

RESULT 179
AAZ90853
ID AAZ90853 standard; DNA; 15 BP.
XX
AC AAZ90853;
XX
DT 24-MAY-2000 (first entry)
XX
DE Human NR8 gene probe #81.
XX
DE Haemopoietin receptor family; NR8; antibody; diagnosis;
KW blood formation disorder; fusion protein; probe; ss.
XX
OS Homo sapiens.
XX
PN W09967290-A1.
XX
PD 29-DEC-1999.
XX
PF 23-JUN-1999; 99WO-JP003351.
XX
PR 24-JUN-1998; 98JP-00214720.
PR 19-OCT-1998; 98JP-00297409.
XX
PA (CHUS ) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX
PI Nomura H, Maeda M;
XX
PF 2000-116933/10.
XX
PT Hemopoietin receptor protein family NR8 used for diagnosis of blood
PT formation disorders.
XX
PS Example 1; Page 41; 176pp; Japanese.
XX
CC The invention relates to the isolation of sequences encoding human
CC haemopoietin receptor protein family NR8 genes. The NR8 family sequences
CC were initially searched for comparison on a nucleic acid database with
CC the nucleic acid probe sequence TGGAGYNNNTGGAGY encoding the amino acid
CC sequence Trp-Ser-Xaa-Trp-Ser. The sequences AAZ9258-Z59300 and AAZ90816-
CC Z90925 represent specific examples of probe sequences used in the search.
CC Antibodies to the NR8 family proteins are used for the diagnosis of blood
CC formation disorders. Compounds identified as binding to the proteins are
CC used for the treatment of such disorders
XX
SQ Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 29 TGGAGTCCTCTGAG 42
      ||||| |||||
Db 1 TGGAGTCCTTGGAG 14

RESULT 180
AAAG3392/c
ID AAAG3392 standard; DNA; 15 BP.
XX
AC AAAG3392;
XX
DT 06-MAR-2001 (first entry)
XX
DE C-1027 gene cluster reverse PCR primer for ORF 12.
XX
KW Enediyne C-1027 biosynthesis gene cluster; apoprotein; chromophore;
KW PCR primer; ss.
XX
OS Streptomyces globisporus.
```


XX WO200040596-A1.
 XX 13-JUL-2000.
 XX 06-JAN-2000; 2000WO-US000446.
 XX 06-JAN-1999; 99US-0115434P.
 XX 05-JAN-2000; 2000US-00477962.
 XX (REGC) UNIV CALIFORNIA.
 XX Shen B, Liu W, Christenson SD, Standage S;
 XX WPI; 2000-465947/40.
 XX Isolated nucleic acid comprising a nucleic acid encoding any of C-1027
 XX open reading frames (ORFs) -7 to 42, excluding ORF 9 (caga), useful for
 XX the production of enediyne C-1027 antitumor antibiotics.
 XX PS Disclosure; Page 17; 160pp; English.
 XX The present invention is concerned with the elucidation of the gene
 XX cluster from Streptomyces globisporus which regulates enediyne C-1027
 XX synthesis. Enediyne C-1027 is an antibiotic, consisting of an apoprotein
 XX and a non-peptidic chromophore, which causes damage to DNA. The primers
 XX AAA63353-A63451 were used to isolate the open reading frames which
 XX comprise the gene cluster. The sequences within the gene cluster can be
 XX used to produce the protein and to identify antagonists, both of which
 XX can be used in the treatment of cancer
 XX SQ Sequence 15 BP; 3 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 AACAAAGCGGCTTG 16
 DB 15 AACAAAGTCGTCCTG 2
 RESULT 181
 AAF49814
 ID AAF49814 standard; DNA; 15 BP.
 XX AC AAF49814;
 XX DT 30-MAR-2001 (first entry)
 XX IGF-I oligonucleotide #774.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 XX hyperneovascular condition; hyperplasia; kidney disease;
 XX neovascular condition of the retina; ss.
 XX Homo sapiens.
 XX WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wraith CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.

PI Wraith CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 XX inhibits or reduces growth factor mediated cell proliferation and/or
 XX inflammation.
 XX Example 8; Page 65; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 XX antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 XX inhibiting or reducing growth factor mediated cell proliferation,
 XX inflammation and/or other disorders. The present sequence is an
 XX oligonucleotide which can be used to design the antisense
 XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
 XX P45161). The method is useful for ameliorating the effects of psoriasis,
 XX ichthyosis, scleroderma, ruba, pilaris, serborrhoea, keloids, keratosis,
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 XX hyperneovascular condition such as a neovascular condition of the retina,
 XX brain or skin, growth factor-mediated malignancies, other sclerotic
 XX disease, kidney disease, hyperproliferation of the inside of blood
 XX vessels or any other hyperplasia
 XX SQ Sequence 15 BP; 4 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 AACAAAGCGGCTTG 16
 DB 2 AACGACACGGCCTG 15
 RESULT 182
 AAF52685
 ID AAF52685 standard; DNA; 15 BP.
 XX AC AAF52685;
 XX DT 30-MAR-2001 (first entry)
 XX IGF-I oligonucleotide #3645.
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 XX hyperneovascular condition; hyperplasia; kidney disease;
 XX neovascular condition of the retina; ss.
 XX Homo sapiens.
 XX WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wraith CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 84; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisenescence oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisenescence
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 GTCTCTGAGAGGT 46
 |||||
 Db 2 GTCTCTGGGAGAT 15

RESULT 183
 AAF49815
 ID AAF49815 standard; DNA; 15 BP.

XX AC AAF49815;

XX DT 30-MAR-2001 (first entry)

XX DE IGF-I oligonucleotide #775.

KW Antisenescence therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 8; Page 66; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisenescence oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisenescence
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 4 A; 5 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AACACAGACGCCCTG 16
 |||||
 Db 1 AACGACACGCCCTG 14

RESULT 184

AAF46719/c

ID AAF46719 standard; DNA; 15 BP.

XX AC AAF46719;

XX DT 30-MAR-2001 (first entry)

XX DE IGFBP3 oligonucleotide #139.

KW Antisenescence therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX Example 7; Page 45; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of

CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like growth factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 AGAGCCAGCGAAGC 62
 DB 15 AGAGTCAGCGCAGC 2
 ||||| ||||| |||||

RESULT 185
 AAF46720/C
 ID AAF46720 standard; DNA; 15 BP.
 XX AC AAF46720;
 XX DT 30-MAR-2001 (first entry)
 XX DB IGFBP3 oligonucleotide #140.
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like growth factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX OS Homo sapiens.
 XX PN WO200078341-A1.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX PS Example 7; Page 45; 201pp; English.
 XX CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like growth factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 1 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 49 AGAGCCAGCGAAGC 62
 DB 14 AGAGTCAGCGCAGC 1
 ||||| ||||| |||||

RESULT 186
 AAF52027
 ID AAF52027 standard; DNA; 15 BP.
 XX AC AAF52027;
 XX DT 30-MAR-2001 (first entry)
 XX DB IGF-I oligonucleotide #2987.
 XX KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like growth factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX OS Homo sapiens.
 XX PN WO200078341-A1.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-AU000693.
 XX PR 21-JUN-1999; 99US-0140345P.
 XX PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX PI Wright CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX PS Example 8; Page 80; 201pp; English.
 XX CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like growth factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTGATG 67
 DB 2 CAGCGTGTGATG 15
 ||||| |||||
 ||||| |||||

RESULT 187
 AAF52686
 ID AAF52686 standard; DNA; 15 BP.
 XX
 AC AAF52686;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGF-I oligonucleotide #3646.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 84; 20pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 2 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 33 GTCCTCTGAGAGGT 46
 DB 1 GTCCTCTGGAGAT 14
 ||||| |||||
 ||||| |||||

RESULT 188
 AAF50644/C
 ID AAF50644 standard; DNA; 15 BP.
 XX
 AC AAF50644;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGF-I oligonucleotide #1604.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 8; Page 71; 20pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 3 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTGATG 67
 DB 15 CGGTGAAGCTGATG 2

RESULT 189

AAF52029

ID AAF52029 standard; DNA; 15 BP.

XX AC AAF52029;

XX DT 30-MAR-2001 (first entry)

XX DE IGF-I oligonucleotide #2989.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX PS Example 8; Page 80; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 2 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 55 AGCGAAGCTGATGT 68
 DB 1 AGCGCTGCTGATGT 14

RESULT 190

AAF50645/C

ID AAF50645 standard; DNA; 15 BP.

XX AC AAF50645;

XX DT 30-MAR-2001 (first entry)

XX DE IGF-I oligonucleotide #1605.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.

XX OS Homo sapiens.

XX PN WO200078341-A1.

XX PD 28-DEC-2000.

XX PF 21-JUN-2000; 2000WO-AU000693.

XX PR 21-JUN-1999; 99US-0140345P.

XX PA (MURD-) MURDOCH CHILDRENS RES INST.

XX PI Wright CJ, Werther GA, Edmondson SR;

XX DR WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.

XX PS Example 8; Page 71; 201pp; English.

XX The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia

XX SQ Sequence 15 BP; 3 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;

Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 54 CAGCGAAGCTGATG 67

DB 14 CGGTGAAGCTGATG 1

RESULT 191
ADV37122/c
ID ADV37122 standard; RNA; 15 BP.
XX
AC ADV37122;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human anti-HER2 NCH ribozyme substrate sequence #954.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 08-NOV-1999; 99US-0156467P.
PR 06-DEC-1999; 99US-00436430.
PR 29-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpaisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
DR WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules
PT obesity and heart disease.
XX
PS Example 7; Page 491; 717pp; English.
XX
CC The present invention relates to the use of enzymatic nucleic acid
CC molecules (e.g. ribozymes) to modulate gene expression. The invention of
CC also methods for their use to down regulate or inhibit the expression of
CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
CC receptor-2 (HER2/c-erbB2/neu), phospholamban (PLN), presenilin-1 (ps-1),
CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
CC nucleic acid molecules used to inhibit the expression of the said genes
CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberyzyme,
CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
CC for treating cancer, in particular breast cancer, Alzheimer's disease,
CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related

CC diseases, hepatitis B infections, and hepatitis and hepatocellular
CC carcinoma. The enzymatic nucleic acid molecules can also be used as
CC diagnostic tools to examine genetic drift and mutations within diseased
CC cells and to detect the presence of specific RNA in a cell. The present
CC sequence represents a substrate/target sequence for an anti-HER2 NCH
CC ribozyme used in the examples of the present invention. Note: Some SEQ ID
CC Nos are repeated more than once in the specification, but these have
CC different sequences associated with them.
XX
SQ Sequence 15 BP; 5 A; 5 C; 4 G; 0 T; 1 U; 0 Other;
Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. NO. 1.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 25 ACTCTGGAGTCCTC 38
Db 14 ACTGTGGGGTCTTC 1
|||||
RESULT 192
ADV35537/c
ID ADV35537 standard; RNA; 15 BP.
XX
AC ADV35537;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human anti-HER2 NCH ribozyme substrate sequence #168.
XX
KW Enzymatic nucleic acid molecule; gene expression; down regulation;
KW protein-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
KW c-erbB2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
KW amberyzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200116312-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-US023998.
XX
PR 31-AUG-1999; 99US-0151713P.
PR 27-SEP-1999; 99US-00406643.
PR 27-SEP-1999; 99US-0156236P.
PR 08-NOV-1999; 99US-0156467P.
PR 06-DEC-1999; 99US-0169100P.
PR 29-DEC-1999; 99US-00474432.
PR 29-DEC-1999; 99US-0173612P.
PR 30-DEC-1999; 99US-00476387.
PR 04-FEB-2000; 2000US-00498824.
PR 20-MAR-2000; 2000US-00531025.
PR 14-APR-2000; 2000US-0197769P.
PR 23-MAY-2000; 2000US-00578223.
PR 09-AUG-2000; 2000US-00636385.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
PI Karpaisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;
PI Stinchcomb D, Beaudry A, Zinnen S, Lugwig J, Sproat BS;
XX
DR WPI; 2001-244406/25.
XX
PT Enzymatic nucleic acid molecules able to cleave separate RNA molecules

PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 XX obesity and heart disease.

Example 7; Page 474; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention of
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
 CC zynzyme, and/or DNazyme motifs. The methods of the invention are useful
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a substrate/target sequence for an anti-HER2 NCH
 CC ribozyme used in the examples of the present invention. Note: Some SEQ ID
 CC Nos are repeated more than once in the specification, but these have
 CC different sequences associated with them.

XX SQ Sequence 15 BP; 1 A; 6 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 ACGGCTGGGGGATA 22

Db 15 ACGGCCAGGGCATA 2

RESULT 193

ADV37121/c
 ID ADV37121 standard; RNA; 15 BP.

XX AC ADV37121;

XX DT 10-FEB-2005 (first entry)

XX DE Human anti-HER2 NCH ribozyme substrate sequence #953.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberzyme; zynzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 KW ss.

XX OS Homo sapiens.

XX FN WO200116312-A2.

XX PD 08-MAR-2001.

XX PP 30-AUG-2000; 2000WO-US023398.

XX PR 31-AUG-1999; 99US-0151713P.

XX PR 27-SEP-1999; 99US-00406643.

XX PR 27-SEP-1999; 99US-0156236P.

XX PR 27-SEP-1999; 99US-0156467P.

XX PR 08-NOV-1999; 99US-00436430.

XX PR 06-DEC-1999; 99US-0169100P.

PR 29-DEC-1999; 99US-00474432.

PR 29-DEC-1999; 99US-0173612P.

PR 30-DEC-1999; 99US-00476387.

PR 04-FEB-2000; 2000US-00498824.

PR 20-MAR-2000; 2000US-00531025.

PR 14-APR-2000; 2000US-0197769P.

PR 23-MAY-2000; 2000US-00578223.

PR 09-AUG-2000; 2000US-00636385.

XX (RIBO-) RIBOZYME PHARM INC.

XX McSwiggen J, Ueman N, Blatt L, Beigelman L, Burgin A;

XX Karpeisky A, Matulic-Adamic J, Svedler D, Draper K, Chowrira B;

XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX WPI; 2001-244406/25.

XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 PT obesity and heart disease.

XX Example 7; Page 491; 717pp; English.

XX The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention of
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),
 CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
 CC zynzyme, and/or DNazyme motifs. The methods of the invention are useful
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a substrate/target sequence for an anti-HER2 NCH
 CC ribozyme used in the examples of the present invention. Note: Some SEQ ID
 CC Nos are repeated more than once in the specification, but these have
 CC different sequences associated with them.

XX SQ Sequence 15 BP; 4 A; 5 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 25 ACTCTGGAGTCTTC 38

Db 15 ACTGTGGGTCTTC 2

RESULT 194

ADV35538/c

ID ADV35538 standard; RNA; 15 BP.

XX AC ADV35538;

XX DT 10-FEB-2005 (first entry)

XX DE Human anti-HER2 NCH ribozyme substrate sequence #169.

XX Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protein-tyrosine-phosphatase-1b; PTB-1B; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberzyme; zynzyme; DNazyme; cancer; breast cancer; Alzheimer's disease;

KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 XX ss.

OS Homo sapiens.

XX WO200116312-A2.

XX 08-MAR-2001.

XX 30-AUG-2000; 2000WO-US023998.

XX 31-AUG-1999; 99US-0151713P.

XX 27-SEP-1999; 99US-00406643.

XX 27-SEP-1999; 99US-0156236P.

XX 27-SEP-1999; 99US-0156467P.

XX 08-NOV-1999; 99US-00436430.

XX 06-DEC-1999; 99US-0169100P.

XX 29-DEC-1999; 99US-00474432.

XX 30-DEC-1999; 99US-0173612P.

XX 04-FEB-2000; 2000US-00476387.

XX 20-MAR-2000; 2000US-00498824.

XX 14-APR-2000; 2000US-00531025.

XX 23-MAY-2000; 2000US-0197769P.

XX 09-AUG-2000; 2000US-00636385.

XX (RIBO-) RIBOZYME PHARM INC.

XX McSwiggen J, Usman N, Blatt L, Beigelman L, Burgin A;

XX Karpaisky A, Matulic-Adamic J, Sweedler D, Draper K, Chowrira B;

XX Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;

XX WPI; 2001-244406/25.

XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules

XX are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,

XX obesity and heart disease.

XX Example 7; Page 474; 71pp; English.

XX The present invention relates to the use of enzymatic nucleic acid

XX molecules (e.g. ribozymes) to modulate gene expression. The invention

XX also methods for their use to down regulate or inhibit the expression of

XX genes encoding protein-tyrosine-phosphatase-1b (PTB-1B), methionine

XX aminopeptidase (MeCAP-2), human telomerase (hTERT), protein kinase C

XX alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor

XX receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),

XX presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic

XX nucleic acid molecules used to inhibit the expression of the said genes

XX include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,

XX zinczyme, and/or DNAzyme motifs. The methods of the invention are useful

XX for treating cancer, in particular breast cancer, Alzheimer's disease,

XX diabetes, obesity, cardiac diseases e.g. heart disease, age-related

XX diseases, hepatitis B infections, and hepatitis and hepatocellular

XX carcinoma. The enzymatic nucleic acid molecules can also be used as

XX diagnostic tools to examine genetic drift and mutations within diseased

XX cells and to detect the presence of specific RNA in a cell. The present

XX sequence represents a substrate/target sequence for an anti-HER2 NCH

XX ribozyme used in the examples of the present invention. Note: Some SEQ ID

XX Nos are repeated more than once in the specification, but these have

XX different sequences associated with them.

XX Sequence 15 BP; 1 A; 5 C; 5 G; 0 T; 4 U; 0 Other;

XX Query Match 14.0%; Score 10.8; DB 1; Length 15;

XX Best Local Similarity 85.7%; Pred. No. 1.3e+02;

XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX QY 9 ACGGCTGGGGATA 22

XX DB 14 ACGGCCAGGGCATA 1

RESULT 195

ABK97479

ID ABK97479 standard; DNA; 15 BP.

XX AC ABK97479;

XX 07-OCT-2002 (first entry)

XX Human LCAT gene polymorphism detection ASO probe #2.

XX Lecithin-cholesterol acyltransferase; LCAT; Norum disease; gene therapy;

XX fish-eye disease; atherosclerotic cardiovascular disease; forensic;

XX population diversity; anthropological lineage; paternity testing; human;

XX polymorphism; allele-specific oligonucleotide; ASO; probe; ss.

XX Homo sapiens.

XX WO200253575-A1.

XX 11-JUL-2002.

XX 03-JAN-2001; 2001WO-US000092.

XX 03-JAN-2001; 2001WO-US000092.

XX (GENA-) GENAISANCE PHARM INC.

XX Chew A, Denton RR, Nandabalan K, Stephens JC;

XX WPI; 2002-557737/59.

XX Novel isolated polymorphic variant polynucleotide of lecithin-cholesterol

XX acyltransferase gene, useful for studying expression and biological

XX function of the gene, and for therapeutic, diagnostic or forensic

XX purposes.

XX Claim 16; Page 16; 72pp; English.

XX The present invention relates to a new polynucleotide comprising a

XX nucleotide sequence which is a polymorphic variant of a reference

XX sequence for lecithin-cholesterol acyltransferase (LCAT). The invention

XX is useful for identifying an association between a trait (preferably a

XX clinical response to drug targeting LCAT) and at least one genotype or

XX haplotype of LCAT gene. The method of the invention has applicability in

XX developing diagnostic tests and therapeutic treatments for Norum disease,

XX fish-eye disease and atherosclerotic cardiovascular disease. The

XX haplotyping and genotyping methods are useful for studying population

XX diversity, anthropological lineage, the significance of diversity and

XX lineage at the phenotypic level, paternity testing, forensic applications

XX and for identifying association between the LCAT genetic variation and a

XX trait such as level of drug response or susceptibility to disease. In

XX addition, the methods for identifying the LCAT haplotypes present in

XX individuals are useful in the development of drugs targeting LCAT. For

XX example, determining the frequency of individual LCAT haplotypes in a

XX population with a specific disease, e.g. Norum disease, will facilitate

XX the development of drugs targeting the LCAT isoform(s) that are most

XX frequent in that disease population. The present nucleic acid sequence

XX represents one of a collection (ABK97478-ABK97491) of allele-specific

XX oligonucleotide (ASO) probes that were used in the invention to detect

XX polymorphisms in the human LCAT gene

XX Sequence 15 BP; 5 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

XX Query Match 14.0%; Score 10.8; DB 1; Length 15;

XX Best Local Similarity 85.7%; Pred. No. 1.3e+02;

XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX QY 52 GCCACGCGAGCTGA 65

XX DB 1 GACAGCTTAGCTGA 14


```

RESULT 198
AEB74336/C
ID AEB74336 standard; RNA; 15 BP.
XX AC AEB74336;
XX AC
XX DT 22-SEP-2005 (first entry)
XX AC ADP47133;
XX DE Hepatitis C virus hammerhead ribozyme substrate sequence.
XX KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
XX KW antiviral; gene therapy; substrate; ss.
XX OS Hepatitis C virus.
XX PN US2002013458-A1.
XX PD 31-JAN-2002.
XX PF 15-FEB-2000; 2000US-00504231.
XX PR 23-MAR-1999; 99US-00274553.
XX PA (BLAT/) BLATT L.
XX PA (MCSW/) MCSWIGGEN J A.
XX PA (ROBE/) ROBERTS E.
XX PA (PAVO/) PAVO P A.
XX PA (MACE/) MACEJACK D.
XX PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX WPI; 2002-215899/27.
XX DR
XX PT New enzymatic nucleic acid molecule, which specifically cleaves minus
XX strand RNA derived from hepatitis C virus, useful for modulating the
XX expression and/or replication of hepatitis C virus.
XX PS Example 1; Page 26; 65pp; English.
XX CC The invention relates to an enzymatic nucleic acid molecule which
XX specifically cleaves minus strand RNA derived from hepatitis C virus
XX (HCV). The binding arms of the molecule comprise ribozyme sequences. The
XX molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
XX Zinzyme motifs. Also described: (1) a pharmaceutical composition
XX comprising the novel enzymatic nucleic acid; (2) a mammalian cell
XX including the novel enzymatic nucleic acid; (3) an expression vector
XX comprising a nucleic acid sequence encoding at least one enzymatic
XX nucleic acid molecule, in a manner, which allows expression of that
XX molecule; (4) a mammalian cell including an expression vector of (3); (5)
XX methods for treating cirrhosis, liver failure or hepatocellular carcinoma
XX by administering to a patient the novel enzymatic nucleic acid or the
XX vector of (3); (6) a method of treating a patient having a condition
XX associated with HCV infection, by contacting cells of the patient with
XX the nucleic acid molecule, and further employing one or more drug
XX therapies; (7) a method for inhibiting HCV replication in a mammalian
XX cell by administering the novel enzymatic nucleic acid; and (8) a method
XX of cleaving a separate RNA molecule by contacting the novel enzymatic
XX nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
XX is useful for modulating the expression and/or replication of hepatitis C
XX virus (HCV), and for inhibiting the expression of HCV minus strand. The
XX nucleic acid may also be used to treat or prevent the occurrence of a
XX disease state in a patient. The present sequence represents an HCV
XX hammerhead ribozyme target substrate sequence which is used in the
XX exemplification of the present invention.
XX SQ Sequence 15 BP; 3 A; 3 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 57 CGAAGCTGATGTC 70

RESULT 199
ADP47133
ID ADP47133 standard; DNA; 15 BP.
XX AC ADP47133;
XX AC
XX DT 09-SEP-2004 (first entry)
XX DE Human phospholipase A2-specific mAb heavy chain DNA sequence #13.
XX KW human; monoclonal antibody; phospholipase A2; PLA2;
XX KW inflammatory disorder; degenerative disorder;
XX KW joint inflammatory reaction; skin inflammatory reaction;
XX KW blood vessels inflammatory reaction; arthritis; psoriasis; asthma;
XX KW Alzheimer's disease; atherosclerosis; restenosis; heavy chain; ds.
XX OS Homo sapiens.
XX PN WO2004050850-A2.
XX PD 17-JUN-2004.
XX PF 02-DEC-2003; 2003WO-US038234.
XX PR 02-DEC-2002; 2002US-0430724P.
XX PA (ABGE-) ABGENIX INC.
XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Landes GM, Haak-Frendscho M, Chen L, Lee YR, Liang ML, Peng X;
XX Jia X, Nocerini MR;
XX WPI; 2004-461119/43.
XX DR
XX PT New human monoclonal antibody that binds to phospholipase A2 (PLA2),
XX useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
XX asthma, Alzheimer's disease, atherosclerosis, or restenosis.
XX PS Example 5; SEQ ID NO 48; 128pp; English.
XX CC The invention comprises a human monoclonal antibody that binds to
XX phospholipase A2 (PLA2). The monoclonal antibody of the invention is
XX useful in the preparation of a medicament for the treatment of
XX inflammatory and degenerative disorders stemming from inflammatory
XX reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
XX asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
XX nucleic acid represents a human PLA2-specific monoclonal antibody heavy
XX chain DNA sequence.
XX SQ Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 14.0%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 GGATCAACTCTGG 31
1 GGATCAGCTATGG 14
Db

RESULT 200
ADP47135
ID ADP47135 standard; DNA; 15 BP.
XX AC ADP47135;
XX AC
XX DT 09-SEP-2004 (first entry)
XX DE Human phospholipase A2-specific mAb heavy chain DNA sequence #15.

```


PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 XX
 PS Example 5; SEQ ID NO 37; 128pp; English.
 XX
 CC The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC nucleic acid represents a human PLA2-specific monoclonal antibody heavy
 CC chain DNA sequence.
 XX
 SQ Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 95.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 18 GGATACAACTCTGG 31
 DB 1 GGATACAGCTATGG 14
 RESULT 203
 AEB19896/c
 ID AEB19896 standard; DNA; 15 BP.
 XX
 AC AEB19896;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE PCR primer #1.
 XX
 KW Microorganism detection; PCR; primer; intestine infection;
 KW gastrointestinal-gen.; gastrointestinal disease; infection; ss.
 XX
 OS Vibrio fluvialis.
 XX
 FN CN1560273-A.
 XX
 PD 05-JAN-2005.
 XX
 PF 26-FEB-2004; 2004CN-00015461.
 XX
 PR 26-FEB-2004; 2004CN-00015461.
 XX
 PA (UYZH-) UNIV ZHONGSHAN.
 XX
 PI Deng X, He J, Wang Z;
 XX
 DR WPI; 2005-296834/31.
 XX
 PT Kit for diagnosing gene of pathogenic bacterial and river vibron of
 PT aquatic animal and human and testing method thereof.
 XX
 PS Claim 1; Page 2; 7pp; Chinese.
 XX
 CC The invention relates to a kit for detecting aquatic animal pathogens and
 CC human pathogens, comprising a pair of PCR primers used to detect specific
 CC DNA fragments of *Vibrio fluvialis*. The kit and method can be used in
 CC bacteria tracking and detection of aquatic animal pathogens in the course
 CC of breeding and also in the clinical detection of human intestinal acute
 CC infections, as well as in environmental monitoring. This sequence
 CC represents a PCR primer used in the scope of the invention.
 XX
 SQ Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 PT useful for treating inflammatory conditions, e.g. arthritis, psoriasis,
 PT asthma, Alzheimer's disease, atherosclerosis, or restenosis.
 XX
 PS Example 5; SEQ ID NO 37; 128pp; English.
 XX
 CC The invention comprises a human monoclonal antibody that binds to
 CC phospholipase A2 (PLA2). The monoclonal antibody of the invention is
 CC useful in the preparation of a medicament for the treatment of
 CC inflammatory and degenerative disorders stemming from inflammatory
 CC reactions in the joints, skin, and blood vessels, arthritis, psoriasis,
 CC asthma, Alzheimer's disease, atherosclerosis, and restenosis. The present
 CC nucleic acid represents a human PLA2-specific monoclonal antibody heavy
 CC chain DNA sequence.
 XX
 SQ Sequence 15 BP; 4 A; 2 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 14.0%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 95.7%; Pred. No. 1.3e+02;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 34 TCCTCTGAGAGGTA 47
 DB 15 TCCTCTGGGAGAA 2
 RESULT 204
 AAN92945
 ID AAN92945 standard; DNA; 12 BP.
 XX
 AC AAN92945;
 XX
 DT 01-JUL-1990 (first entry)
 XX
 DE Consensus sequence for mammalian expression vector.
 XX
 KW Murine autonomously replicating sequence; consensus sequence;
 KW mammalian expression vector.
 XX
 OS Mouse.
 XX
 PN EP306848-A.
 XX
 PD 15-MAR-1989.
 XX
 PF 02-SEP-1988; 88EP-00114317.
 XX
 PR 09-SEP-1987; 87DE-03730246.
 XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Grummt F, Weidle U;
 XX
 DR WPI; 1989-078357/11.
 XX
 PT Expression vectors for mammalian cells - with two consensus sequences and
 PT inefficient selection system.
 XX
 PS Claim 2; Page 8; 12pp; German.
 XX
 CC The inventors claim vectors for the expression of heterologous proteins
 CC in mammalian cells. Each vector has a first and second consensus sequence
 CC (CS). The CS or their homologues are present in known murine autonomously
 CC replicating sequences (MuARS). The first CS is homologous to AAN92945.
 CC The inefficient selection system comprises the tk gene and a truncated tk
 CC promoter. The vectors also contain a gene coding for a protein and the
 CC necessary promoter and terminator sequences for the expression of this
 CC gene. The expression vectors provide rapid amplification, allow selection
 CC of best clones in a short time, are of universal utility in mammalian
 CC cells, and are free of viral origin sequences
 XX
 SQ Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 13.5%; Score 10.4; DB 1; Length 12;
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 36 CTCTGAGAGGTA 47
 DB 1 CTCTGAGAGAA 12
 RESULT 205
 ABI24047/c
 ID ABI24047 standard; DNA; 12 BP.
 XX
 AC ABI24047;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 324020 for detecting SNP TSC0031735.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 324020; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 0 A; 6 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 13.5%; Score 10.4; DB 1; Length 12;
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 50 GAGCCAGCGAAG 61
 Db 12 GAGCGAGCGAAG 1
 |||||
 RESULT 206
 ABH85885/c
 ID ABH85885 standard; DNA; 12 BP.
 XX
 AC ABH85885;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide primer SEQ ID NO 285878 for detecting SNP TSC0012487.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA

XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 285878; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 12 BP; 1 A; 4 C; 0 G; 7 T; 0 U; 0 Other;
 Query Match 13.5%; Score 10.4; DB 1; Length 12;
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 40 GAGAGGTAAAGA 51
 Db 12 GAGAGGTAAAGA 1
 |||||
 RESULT 207
 ABH17646
 ID ABH17646 standard; DNA; 12 BP.
 XX
 AC ABH17646;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide primer SEQ ID NO 317619 for detecting SNP TSC0028141.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 317619; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 12;
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 41 AGAGGTAAGAG 52
 Db 1 AAAGGTAAGAG 12
 |||||

RESULT 208
 ABI18779
 ID ABI18779 standard; DNA; 12 BP.
 AC ABI18779;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX
 DE Oligonucleotide primer SEQ ID NO 318752 for detecting SNP TSC0028845.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 318752; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 12 BP; 6 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 12;
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAG 50
 Db 1 TGAGAGATAAG 12
 |||||

RESULT 209
 ABI33596/C
 ID ABI33596 standard; DNA; 12 BP.
 XX
 AC ABI33596;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX
 DE Oligonucleotide primer SEQ ID NO 333569 for detecting SNP TSC0037605.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 333569; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 12 BP; 2 A; 4 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 12;
 Best Local Similarity 91.7%; Pred. No. 1.2e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAAG 50
 Db 12 TGAGAGATAAG 1
 |||||

RESULT 210
 AAX22517
 ID AAX22517 standard; RNA; 13 BP.
 XX

```

AC AAX22517;
XX
XX 25-MAR-2003 (revised)
DT 21-MAY-1999 (first entry)
XX
XX Streptomyces sp. aac7 gene RBS RNA fragment.
DE
XX
XX Xylanase; acidophilic; thermostable; XYL I; XYL II; plant biomass;
KW hemicellulase; beta-1,4 bond; xylosic chain; xylan; D-xylose; paper;
KW pulp; chlorine bleaching; feed; beta-glucan; cellulose; lignin; ds.
XX
XX Streptomyces sp.
OS
XX
XX US5871730-A.
PN
XX
XX 16-FEB-1999.
PD
XX
XX 29-JUL-1994; 94US-00282197.
PF
XX
XX 29-JUL-1994; 94US-00282197.
PR
XX
XX (UYSH ) UNIV SHERBROOKE.
PA
XX
XX Beaulieu C, Brzezinski R, Dery CV;
PI
XX WPI; 1996-141348/14.
DR
XX
XX New acidophilic and thermostable xylanase enzymes from Actinomadura sp.
XX FC7 - useful for treating plant biomass, especially paper and wood pulp,
PT to degrade hemicellulose and hydrolyse xylan.
PT
XX
XX Example 7; Fig 7; 60pp; English.
PS
XX
XX This invention describes the use of novel acidophilic and thermostable
CC xylanase enzymes (XYL I and XYL II) from Actinomadura sp. FC7 which
CC retain their activity under harsh industrial conditions (e.g. high
CC temperature or wide pH ranges) and may be secreted by recombinant host
CC cells, to treat plant biomass. Xylanases XYL I and XYL II are part of a
CC large group of hemicellulase enzymes and function by cutting the beta-1,4
CC bonds within the xylosic chain of xylan (a polymer of D-xylose residues
CC that is a major constituent of hemicellulose). This means that they may
CC be used in the paper and pulp industry to improve the efficiency of the
CC bleaching process by degrading the structure of the material. XYL I and
CC XYL II may also be used to treat feed, by degrading a substrate with a
CC high beta-glucan or cellulose content. XYL I and XYL II retain their
CC activity at high temperatures (e.g. 70 deg. C) and at low pHs (e.g. 4.0),
CC conditions which tend to denature most known xylanases. Enzymes that
CC remain active in these conditions may be used in industrial processes
CC that are carried out at high temperature and low pH to speed up other,
CC non-enzymatic reactions, minimising costs, energy requirements, and the
CC risk of pollution, (e.g. enzymes XYL I and XYL II can be used to
CC facilitate chlorine bleaching of paper pulp which is carried out in hot,
CC acidic conditions). Pretreatment with XYL I and XYL II, allows the
CC bleaching agents to penetrate better, to remove lignin from the pulp and
CC 'bleach' the colouration from it. This means smaller quantities of the
CC agents can be used to produce the same or a better result. Also,
CC disrupting the structure aids water drainage. NOTE: This patent is an
CC equivalent to FI9503640. (Updated on 25-MAR-2003 to correct DR field.)
XX
XX Sequence 13 BP; 2 A; 4 C; 5 G; 0 T; 2 U; 0 Other;
SQ
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 56 GCGAAGCTGATG 67
Db 2 GCGACGCGAUG 13

RESULT 211
AAC88504
ID AAC88504 standard; RNA; 13 BP.

AAC88504;
02-MAR-2001 (first entry)
Murine pl6 coding sequence fragment.
Ribozyme; retinal degradation; retinal disease; learning; memory;
amyotrophic lateral sclerosis; tumour suppression; ss.
Mus sp.
WO200066780-A2.
09-NOV-2000.
28-APR-2000; 2000WO-US011509.
30-APR-1999; 99US-0131942P.
(UYFL ) UNIV FLORIDA.
Lewin AS, Muzyczka N, Hauswirth WM, Teschendorf C, Burger C;
WPI; 2000-687548/67.
Novel methods for identifying genes with selected functions comprising
contacting genes with a library of ribozymes, useful for identifying
genes involved in, e.g. retinal disease, learning or memory and tumor
suppression.
Claim 16; Fig 7; 111pp; English.
The present invention relates to a method for identifying a gene with a
selected function comprising contacting genes with a library of ribozymes
and identifying at least 1 ribozyme that alters the selected function of
the gene. The present sequence is a target sequence used in the present
invention. The methods (and ribozymes) are useful for identifying novel
genes involved in retinal degradation, retinal disease, learning or
memory, amyotrophic lateral sclerosis or tumour suppression, and for
producing non-human animal models of diseases
Sequence 13 BP; 1 A; 4 C; 5 G; 0 T; 3 U; 0 Other;
SQ
Query Match 13.5%; Score 10.4; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 29 TCGAGTCCTCTG 40
Db 1 UGGAGUCCGUG 12

RESULT 212
ABH39407/C
ID ABH39407 standard; DNA; 13 BP.
AC ABH39407;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 239384 for detecting SNP TSC0058391.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX

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CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 2 A; 7 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match      13.5%; Score 10.4; DB 1; Length 13;
  Best Local Similarity 91.7%; Pred. No. 1.3e+02;
  Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTTAAAG 50
Db 13 TGAGAGGTTAAG 2

RESULT 215
ABH04743/C
ID ABH04743 standard; DNA; 13 BP.
XX
XX ABH04743;
AC
AC ABH04743;
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 204720 for detecting SNP TSC0050222.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
DT
XX
XX 06-APR-2001; 2001WO-IB000713.
DE
XX
XX 07-APR-2000; 2000DE-01019173.
DT
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX
XX Claim 1; SEQ ID NO 204720; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 6 C; 0 G; 4 T; 0 U; 1 Other;

  Query Match      13.5%; Score 10.4; DB 1; Length 13;
  Best Local Similarity 91.7%; Pred. No. 1.3e+02;
  Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTTAAAG 50
Db 13 TGAGAGGTTAAG 2

RESULT 216
ABH39406
ID ABH39406 standard; DNA; 13 BP.
XX
XX ABH39406;
AC
AC ABH39406;
XX
XX 22-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 239383 for detecting SNP TSC0058391.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
OS
XX
XX WO200177384-A2.
PN
XX
XX 18-OCT-2001.
DT
XX
XX 06-APR-2001; 2001WO-IB000713.
DE
XX
XX 07-APR-2000; 2000DE-01019173.
DT
XX
XX (EPIG-) EPIGENOMICS AG.
PA
XX
XX Olek A, Piepenbrock C, Berlin K;
PI
XX
XX WPI; 2001-657177/75.
DR
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
PT
XX
XX Claim 1; SEQ ID NO 239383; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 6 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match      13.5%; Score 10.4; DB 1; Length 13;
  Best Local Similarity 91.7%; Pred. No. 1.3e+02;
  Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 TGAGAGGTTAAAG 50
Db 2 TGAGAGGTTAAG 13

RESULT 217
ABF32920
ID ABF32920 standard; DNA; 13 BP.
XX
XX ABF32920;
AC
AC ABF32920;
XX
XX 21-FEB-2002 (first entry)
DT
XX
XX Oligonucleotide SEQ ID NO 132917 for detecting SNP TSC0033164.
DE
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

```

KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 139917; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 13.5%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 39 TGAGAGGTTAAAG 50
 Db 2 TGAGAGGTTAAAG 13
 |||||
 RESULT 218
 ABP95653/C
 ID ABP95653 standard; DNA; 13 BP.
 XX
 AC ABP95653;
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide SEQ ID NO 195650 for detecting SNP TSC0048132.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 195650; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 5 C; 0 G; 6 T; 0 U; 0 Other;
 Query Match 13.5%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 41 AGAGGTTAAAGAG 52
 Db 13 AGAGGTTAAAGTG 2
 |||||
 RESULT 219
 ABH04742
 ID ABH04742 standard; DNA; 13 BP.
 XX
 AC ABH04742;
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide SEQ ID NO 204719 for detecting SNP TSC0050222.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX WO200177384-A2.
 PN 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 PR (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 XX designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX Claim 1; SEQ ID NO 204719; 29pp + Sequence Listing; German.
 PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 4 A; 0 C; 6 G; 2 T; 0 U; 1 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 39 TGAGAGGTAAAG 50
 Db 1 TGAGAGGTAGAG 12

RESULT 220
 ABC36749/c
 ID ABC36749 standard; DNA; 13 BP.
 AC ABC36749;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 36766 for detecting SNP TSC0011511.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 36766; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 1 A; 4 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGAG 52
 Db 12 AAAGGTAAAGAG 1

RESULT 221
 ABF13387/c
 ID ABF13387 standard; DNA; 13 BP.
 XX
 AC ABF13387;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 113384 for detecting SNP TSC0028368.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 113384; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 13 BP; 0 A; 7 C; 0 G; 6 T; 0 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 13;
 Best Local Similarity 91.7%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 41 AGAGGTAAAGAG 52
 Db 13 AGAGGGAAAGAG 2

RESULT 222
 ABC36748
 ID ABC36748 standard; DNA; 13 BP.
 XX

Query Match 13.5%; Score 10.4; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. NO. 1.4e+02;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 62 CTGATGTCCTGT 73
 |:|:|:|:|:
 Db 1 CUGCUGCCUGU 12

RESULT 227
 AEB01535
 ID AEB01535 standard; RNA; 14 BP.
 XX
 AC AEB01535;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Hepatitis C virus substrate #20 for HCV hairpin ribozyme #20.
 XX
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytostatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hairpin ribozyme; HP ribozyme; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN US2002082225-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 23-MAR-1999; 99US-00274553.
 XX
 PR 23-MAR-1999; 99US-00274553.
 XX
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA (ROBE/) ROBERTS B.
 PA (PAVC/) PAVCO P A.
 PA (MACE/) MACEJACK D.
 XX
 PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;
 XX WPI; 2002-617759/66.
 XX
 DR New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
 XX replication and are useful to treat hepatitis C virus infections and
 XX cirrhosis, liver failure or hepatocellular carcinoma.
 XX
 PS Claim 2; Page 59; 80pp; English.
 XX
 CC The present invention relates to enzymatic nucleic acids which
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
 CC (HP) motif where the binding arms comprise sequences complementary to one
 CC of the substrate sequences defined in the specification. The HCV
 CC ribozymes are useful for modulating the expression and/or replication of
 CC HCV. They can be used to treat cirrhosis, liver failure and/or
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
 CC a condition associated with HCV infection in conjunction with one or more
 CC other drug therapies, particularly type I interferon, especially
 CC interferon alpha, beta or gamma or consensus interferon. The present
 CC sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note:
 CC Some of the sequence data for this patent did not form part of the
 CC printed specification. The complete sequence data for this patent was
 CC obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipsdIDEntry.html
 XX
 SQ Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. NO. 1.4e+02;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 62 CTGATGTCCTGT 73
 |:|:|:|:|:
 Db 1 CUGCUGCCUGU 12

RESULT 228
 AEB76459
 ID AEB76459 standard; RNA; 14 BP.
 XX
 AC AEB76459;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Hepatitis C virus hairpin ribozyme substrate sequence.
 XX
 KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
 KW antiviral; gene therapy; substrate; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN US2002013458-A1.
 XX
 PD 31-JAN-2002.
 XX
 PF 15-FEB-2000; 2000US-00504231.
 XX
 PR 23-MAR-1999; 99US-00274553.
 XX
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA (ROBE/) ROBERTS E.
 PA (PAVC/) PAVCO P A.
 PA (MACE/) MACEJACK D.
 XX
 PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
 XX WPI; 2002-215899/27.
 XX
 DR New enzymatic nucleic acid molecule, which specifically cleaves minus
 XX strand RNA derived from hepatitis C virus, useful for modulating the
 XX expression and/or replication of hepatitis C virus.
 XX
 PS Example 1; Page 43; 65pp; English.
 XX
 CC The invention relates to an enzymatic nucleic acid molecule which
 CC specifically cleaves minus strand RNA derived from hepatitis C virus
 CC (HCV). The binding arms of the molecule comprise ribozyme sequences. The
 CC molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
 CC Zinzyne motifs. Also described: (1) a pharmaceutical composition
 CC comprising the novel enzymatic nucleic acid; (2) a mammalian cell
 CC including the novel enzymatic nucleic acid; (3) an expression vector
 CC comprising a nucleic acid sequence encoding at least one enzymatic
 CC nucleic acid molecule, in a manner, which allows expression of that
 CC molecule; (4) a mammalian cell including an expression vector of (3); (5)
 CC methods for treating cirrhosis, liver failure or hepatocellular carcinoma
 CC by administering to a patient the novel enzymatic nucleic acid or the
 CC vector of (3); (6) a method of treating a patient having a condition
 CC associated with HCV infection, by contacting cells of the patient with
 CC the nucleic acid molecule, and further employing one or more drug
 CC therapies; (7) a method for inhibiting HCV replication in a mammalian
 CC cell by administering the novel enzymatic nucleic acid; and (8) a method
 CC of cleaving a separate RNA molecule by contacting the novel enzymatic
 CC nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
 CC is useful for modulating the expression and/or replication of hepatitis C
 CC virus (HCV), and for inhibiting the expression of HCV minus strand. The
 CC nucleic acid may also be used to treat or prevent the occurrence of a
 CC disease state in a patient. The present sequence represents an HCV
 CC hairpin ribozyme target substrate sequence which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 13.5%; Score 10.4; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 62 CTGATGTCCTGT 73
 DB 1 CUGCUGUCCUGU 12

RESULT 229
 AAQ47917
 ID AAQ47917 standard; DNA; 10 BP.
 XX
 AC AAQ47917;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-MAR-1994 (first entry)
 XX
 DE Primer for production of cDNA from mRNA.
 XX
 KW cDNA; mRNA; primer; PCR; polymerase chain reaction; poly A site; RT;
 KW reverse transcriptase; kozak sequence; ss.
 XX
 OS Synthetic.
 XX
 PN WO9318176-A1.
 XX
 PD 16-SEP-1993.
 XX
 PF 11-MAR-1993; 93WO-US002246.
 XX
 PR 11-MAR-1992; 92US-00850343.
 PR 11-MAR-1993; 93US-00033084.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Liang P, Pardee AB;
 XX
 DR WPI; 1993-303488/38.
 XX
 PT Cloning and isolating mRNA as cDNA - by reverse transcription and
 PT polymerase amplification using two oligo-deoxy-nucleotide(s).
 XX
 PS Example 4; Page 17; 43pp; English.
 XX
 CS Two primers are used to amplify any given mRNA molecule in its cDNA form.
 CC The first primer is capable of binding either to (1) a site immediately
 CC upstream of the first adenine nucleotide of the poly A tail; (2) to a
 CC site including the mRNA's poly A signal sequence; (3) to a site including
 CC the mRNA's Kozak sequence or (4) to a sequence of an mRNA of which the
 CC nucleotide sequence is known. These primers are then extended by reverse
 CC transcriptase to produce the corresponding cDNA sequence. The second
 CC primer comprises an arbitrary sequence and is used alongside the first
 CC primer to amplify the cDNA molecule by PCR. This primer is a second
 CC arbitrary primer. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
 DB 1 AGCCAGCGAA 10

RESULT 231
 AAT18616
 ID AAT18616 standard; DNA; 10 BP.
 XX
 AC AAT18616;
 XX
 DT 06-NOV-1996 (first entry)
 XX
 DE Arbitrary 5' oligodecamer DDRT-PCR primer OPA 16.
 XX
 KW Differential display of mRNA; reverse transcription; DDRT-PCR; human;
 KW chondrocyte; gene specific; primer; probe; isolation; interleukin-1beta;
 KW IL-1beta; diagnosis; connective tissue disease; osteoarthritis;
 KW rheumatoid arthritis; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN EF705842-A2.
 XX
 PD 10-APR-1996.
 XX
 PF 02-OCT-1995; 95EP-00115510.
 XX

Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
 DB 1 AGCCAGCGAA 10

RESULT 230
 AAQ99394
 ID AAQ99394 standard; DNA; 10 BP.
 XX
 AC AAQ99394;

XX
 DT 12-FEB-1996 (first entry)
 XX
 DE Syngeneic and allogeneic transplant comparison primer, OPA-16.
 XX
 KW AIF-1; allograft inflammatory factor 1; transplant rejection; inhibitor;
 KW immunogenic; detection; diagnosis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9517506-A1.
 XX
 PD 29-JUN-1995.
 XX
 PF 21-DEC-1994; 94WO-US014724.
 XX
 PR 21-DEC-1993; 93US-00171385.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Russell ME, Utans U;
 XX
 DR WPI; 1995-240668/31.
 XX
 PT DNA encoding allograft rejection factors and immunogenic fragments -
 PT useful for identifying transplant rejection inhibitors.
 XX
 PS Disclosure; Page 12; 138pp; English.
 XX
 CS AAQ99394-Q99396 are primers used to identify DNA from both allogeneic and
 CC syngeneic sources to determine where a specific gene is expressed. The
 CC AIF-1 gene is a differentially expressed allograft gene which is
 CC expressed in allograft tissue during transplant rejection. Identification
 CC of the AIF-1 product (AAR80520) or transcript indicates that allograft
 CC rejection is taking place. The human AIF-1 gene and product are therefore
 CC useful in the diagnosis of transplant rejection. The diagnostic methods
 CC used allow rejection (vascular inflammation) to be detected at an early
 CC stage and require only a small amount of biopsy material
 XX
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
 DB 1 AGCCAGCGAA 10

RESULT 231
 AAT18616
 ID AAT18616 standard; DNA; 10 BP.
 XX
 AC AAT18616;
 XX
 DT 06-NOV-1996 (first entry)
 XX
 DE Arbitrary 5' oligodecamer DDRT-PCR primer OPA 16.
 XX
 KW Differential display of mRNA; reverse transcription; DDRT-PCR; human;
 KW chondrocyte; gene specific; primer; probe; isolation; interleukin-1beta;
 KW IL-1beta; diagnosis; connective tissue disease; osteoarthritis;
 KW rheumatoid arthritis; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN EF705842-A2.
 XX
 PD 10-APR-1996.
 XX
 PF 02-OCT-1995; 95EP-00115510.
 XX

```

PR 06-OCT-1994; 94BP-00115751.
XX (PARH ) HOECHST AG.
XX Bartnik E, Margerie D;
PI WPI; 1996-181045/19.
XX
XX Diagnosis and treatment of IL-1 mediated connective tissue diseases -
PT using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or
PT antibodies to them.
XX
XX Example; Page 15; 31pp; English.
XX
XX The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which
CC were used along with 4 degenerate 3' oligo dt primers for the
CC differential display of human chondrocyte mRNA by reverse transcription
CC and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA
CC clones, which were then searched against DNA databases for homology to
CC known human genes. The cDNA mols. can be used for the prodn. of gene
CC specific primers and probes to isolate genes induced by treating (esp.
CC human) chondrocytes with interleukin-1beta (IL-1beta), and for the
CC diagnosis of IL-1beta related connective tissue diseases, in partic.
CC osteoarthritis or rheumatoid arthritis
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 51 AGCCAGCGAA 60
DB 1 AGCCAGCGAA 10
|||||
RESULT 232
AAT75144
ID AAT75144 standard; DNA; 10 BP.
XX
XX AAT75144;
AC
XX
XX 04-MAR-1998 (first entry)
DT Arbitrary RT-PCR primer.
DE
XX
XX dhc-1; homocysteine; hypohomocysteinaemia; atherosclerosis; diagnosis;
KW serum; Dami cell; PCR; arbitrary primer; messenger RNA pool; ss.
XX
XX Synthetic.
OS
XX
XX WO9725440-A2.
FN
XX
XX 17-JUL-1997.
PD
XX
XX 02-JAN-1997; 97WO-CA000001.
PF
XX
XX 03-JAN-1996; 96US-00582261.
PR (HAMI-) HAMILTON CIVIC HOSPITALS RES DEV INC.
XX
XX Austin RC, Hirsch J, Weitz J;
PI WPI; 1997-372877/34.
XX
XX Methods and polynucleotide(s) for diagnosing hyperhomocysteinaemia -
PT and/or predisposition to develop premature atherosclerosis by detecting
PT increased levels of serum homocysteine.
XX
XX Disclosure; Page 22; 84pp; English.
PS
XX Arbitrary RT-PCR primers (AAT75138-42) were used to amplify mRNA from
CC cells exposed to hyperphysiological, normal or subphysiological levels of
CC

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```

CC homocysteine. PCR products were separated on a sequencing gel and
CC discrete fractions which were increased or decreased were identified.
CC This method was used to identify mRNA and the corresponding cDNA which
CC are increased in the cells of a patient having hyperhomocysteinaemia or a
CC predisposition to homocysteine mediated atherosclerosis. These
CC polynucleotides can be used for the diagnosis and treatment of
CC atherosclerotic diseases and diseases of metabolism of sulphur containing
CC amino acids (e.g. homocysteinaemia), which are associated with vascular
CC damage and atherosclerotic disease, specifically unstable angina, acute
CC myocardial infarction (heart attack), cerebrovascular accidents (stroke),
CC hypertension, renal artery stenosis, aortic stenosis and deep vein
CC occlusive disease
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 51 AGCCAGCGAA 60
DB 1 AGCCAGCGAA 10
|||||
RESULT 233
AAV10688
ID AAV10688 standard; DNA; 10 BP.
XX
XX AAV10688;
AC
XX
XX 21-JUL-1998 (first entry)
DT Human breast cancer gene differential display primer #6.
DE
XX
XX Breast cancer; malignant transformation; diagnostic; therapeutic;
KW screening; primer; ss.
XX
XX Synthetic.
OS
XX
XX Homo sapiens.
XX
XX WO9738085-A2.
FN
XX
XX 16-OCT-1997.
PD
XX
XX 09-APR-1997; 97WO-US005930.
PF
XX
XX 10-APR-1996; 96US-0015167P.
PR 05-JUN-1996; 96WO-US009286.
PR 06-JUN-1996; 96US-0019202P.
PR 11-JUL-1996; 96US-00678280.
XX
XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
PA
XX
XX Smith H, Chen L;
PI WPI; 1997-512705/47.
XX
XX Breast cancer genes - used to develop products to design or screen
PT diagnostic reagents or therapeutic compounds.
XX
XX Example 2; Page 46; 118pp; English.
XX
XX Primers AAV10683-V10688 are used to obtain novel human breast cancer
CC genes by differential display. The identified genes or fragments of these
CC genes can be used for identifying genes and gene products that are
CC intimately related to malignant transformation or maintenance of the
CC malignant properties of cancer cells. It can also be used to design or
CC screen diagnostic reagents or therapeutic compounds. Kits are included
CC within the scope of the invention
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
SQ
Query Match 13.0%; Score 10; DB 1; Length 10;

```


Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0;

QY 51 AGCCAGCGAA 60
 |||||
 Db 1 AGCCAGCGAA 10

RESULT 234
 AAV15590
 ID AAV15590 standard; DNA; 10 BP.
 AC AAV15590;
 XX
 DT 02-JUL-1998 (first entry)
 XX
 DE Human HPK-1A C4.8 and C21.7 PCR primer AP-1.
 XX
 KW Cervical cancer; treatment; diagnosis; passage cell; lesion;
 KW human foreskin keratinocyte cell line; HPK-1A; antibody; smear;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN DE19649207-C1.
 XX
 PD 26-FEB-1998.
 XX
 XX 27-NOV-1996; 96DE-01049207.
 XX
 PR 27-NOV-1996; 96DE-01049207.
 XX
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA
 XX Duerst M, Nees M;
 PI
 XX WPI; 1998-121623/12.
 DR
 XX Nucleic acid characteristic of late or early passage cells immortalised
 PT by papilloma virus - and related polypeptide(s) and antibodies, used for
 PT diagnosis and treatment of cervical cancer and assessing potential for
 PT progression of cervical lesions.
 XX
 PS Example 1; Page 4; 8pp; German.
 XX
 CC PCR primers AAV15590 and AAV15591 are used to amplify fragments of the
 CC C4.8 and C21.7 genes from a human papillomavirus (HPV) immortalised human
 CC foreskin keratinocyte cell line HPK-1A. These genes are characteristic of
 CC late or early passage cells and can be used in a method for assessing the
 CC potential for progression of cervical lesions. Antibodies generated
 CC against the encoded polypeptide are used for diagnosis of cervical cancer
 CC and to assess potential for lesion progression. Antibodies can also be
 CC used therapeutically by inhibiting the polypeptide. Antisense molecules
 CC based on the nucleotide sequence are used to inhibit expression of the
 CC protein. Detecting polypeptides, or related RNA, characteristic of late
 CC passage cells (which are potentially malignant) in cervical smears is a
 CC reliable way of assessing progression potential
 XX
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
 |||||
 Db 1 AGCCAGCGAA 10

RESULT 235
 AAX34945
 ID AAX34945 standard; DNA; 10 BP.

XX AAX34945;
 AC
 DT 28-JUN-1999 (first entry)
 XX
 DE PCR primer for DNA encoding a dehiscence zone protein ORS7(9).
 KW Dehiscence zone protein; ORS7(9); regulation; pod dehiscence;
 KW plant abscission; PCR primer; ss.
 XX
 OS Synthetic.
 OS Brassica napus.
 XX
 FN WO9915680-A1.
 XX
 PD 01-APR-1999.
 XX
 PP 18-SEP-1998; 98WO-GB002836.
 XX
 PR 19-SEP-1997; 97GB-00020038.
 XX
 PA (BIOG-) BIOGEMMA UK LTD.
 XX
 PI Paul W, Roberts JA, Whitelaw C;
 XX
 DR WPI; 1999-244427/20.
 XX
 PT New Brassica napus nucleic acid and protein, useful for regulating pod
 PT dehiscence and/or plant abscission by producing transgenic plants or
 PT propagating material.
 XX
 PS Example 1; Page 10; 20pp; English.
 XX
 CC PCR primer AAX34944-45 were used to amplify DNA encoding a dehiscence
 CC zone protein designated ORS7(9). The ORS7(9) polynucleotides and
 CC polypeptides are useful for regulating pod dehiscence and plant
 CC abscission. Antisense ORS7(9) nucleic acid useful for preventing or
 CC reducing dehiscence or abscission
 XX
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 AGCCAGCGAA 60
 |||||
 Db 1 AGCCAGCGAA 10

RESULT 236
 AAZ22961
 ID AAZ22961 standard; DNA; 10 BP.
 XX
 AC AAZ22961;
 XX
 DT 10-JAN-2000 (first entry)
 XX
 DE Arbitrary primer A.
 XX
 KW Signal transduction protein; dehiscence; male sterile plant;
 KW shatter resistance; oilseed rape; primer; ss.
 XX
 OS Synthetic.
 XX
 FN WO9949046-A1.
 XX
 PD 30-SEP-1999.
 XX
 PP 22-MAR-1999; 99WO-GB000905.
 XX
 PR 20-MAR-1998; 98GB-00006113.
 XX

PA (BIOG-) BIOGENMA UK LTD.
 XX Wyatt P, Roberts JA, Whitelaw C;
 XX WPI; 1999-580449/49.
 DR A nucleic acid encoding a signal transduction protein involved in plant
 PT dehiscence, useful for producing shatter resistant male sterile plants.
 XX Example 1; Page 23; 71pp; English.
 XX The invention provides a nucleic acid encoding a signal transduction
 CC protein involved in the process of dehiscence. The nucleic acids and
 CC proteins are useful for regulating or controlling dehiscence of a pod or
 CC an anther in a plant, useful in the production of male sterile plants.
 CC The methods, etc. may be used in production of shatter resistance or
 CC shatter-delayed plants such as oilseed rape (*Brassica napus*)
 XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 SQ Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 51 AGCCAGCGAA 60
 Db 1 AGCCAGCGAA 10
 |||||
 RESULT 237
 AAX26829
 ID AAX26829 standard; DNA; 10 BP.
 XX AAX26829;
 AC
 XX 22-JUN-1999 (first entry)
 DT PCR primer AP-1 used to amplify Rin2 cDNA sequences.
 DE Rin2; downregulation; functional response; allergy; asthma; hayfever;
 XX Ras-dependent signalling pathway; allergy; asthma; hayfever;
 KW atopic eczema; Ras-dependent cancer; neoplastic cellular proliferation;
 KW autoimmune disease; T cell-associated disease;
 KW T cell dependent graft vs. host disease; type I diabetes mellitus;
 KW multiple sclerosis; Crohn's disease; autoimmune hepatitis; psoriasis;
 KW wound healing; angiogenesis; re-epithelialization;
 KW human immune deficiency virus; immune suppression; cancer therapy;
 KW nerve regeneration; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO9913079-A1.
 PN 18-MAR-1999.
 XX 11-SEP-1998; 98WO-US019056.
 PF 11-SEP-1997; 97US-0058520P.
 PR 02-OCT-1997; 97US-00942819.
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA Tam S, Tsai M, Galli SJ;
 PI WPI; 1999-229239/19.
 DR Rin2 polypeptides and related nucleic acid.
 XX Disclosure; Page 47; 101pp; English.
 PS The present sequence represents a primer used to amplify Rin2 cDNA
 CC sequences. Rin2 polypeptides downregulate functional responses elicited
 CC by Ras-dependent signalling pathways. Agents that increase Rin2 activity

CC (particularly Rin2 itself, optionally expressed from a vector) are used
 CC to treat allergy (asthma, hayfever or atopic eczema); Ras-dependent
 CC cancers and (non-)neoplastic cellular proliferation; autoimmune diseases;
 CC T cell-associated diseases and T cell dependent graft vs. host disease
 CC (typical examples being type I diabetes mellitus; multiple sclerosis;
 CC Crohn's disease, autoimmune hepatitis and psoriasis). Agents that inhibit
 CC Rin2 activity are used to improve wound healing; angiogenesis and/or re-
 CC epithelialization (also to improve immune response to pathogens; in human
 CC immune deficiency virus, and some other, infections; immune suppression
 CC associated with cancer therapy, and nerve regeneration)
 XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 SQ Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 51 AGCCAGCGAA 60
 Db 1 AGCCAGCGAA 10
 |||||
 RESULT 238
 AAZ25357
 ID AAZ25357 standard; DNA; 10 BP.
 XX AAZ25357;
 AC
 XX 17-DEC-1999 (first entry)
 DT Rat DRM PCR primer #1.
 DE DRM; secreted protein; cell growth inhibition; fusion protein; tumour;
 XX green fluorescent protein; GFP; hyperproliferative cell disorder;
 KW enhanced green fluorescent protein; EGFP; diagnosis; PCR primer; ss.
 XX Synthetic.
 OS
 XX Rattus sp.
 XX WO9949041-A1.
 PN 30-SEP-1999.
 PD 26-MAR-1999; 99WO-US006675.
 PF 26-MAR-1998; 98US-0079440P.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA Blair DG, Clausen PA, Topol LZ, Marx M, Calothy G;
 PI WPI; 1999-591095/50.
 DR New isolated nucleic acid encoding DRM protein, for regulation of cell
 XX growth, particularly treating cancer and.
 PT Example 1; Page 31; 115pp; English.
 PS The present invention describes nucleic acids comprising human, murine or
 CC rat cDNAs encoding DRM proteins (derived from the down-regulated in v-mos
 CC -transformed cells, drm gene). The nucleic acids, and DRM proteins, are
 CC useful for arresting cell growth; inhibiting tumour cell growth; treating
 CC hyperproliferative cellular disorders, either in vivo or ex vivo and
 CC producing fusion proteins with enhanced green fluorescent protein (EGFP)
 CC of increased stability (useful in screening assays, protein-protein
 CC interaction studies, cell labeling and as markers during purification).
 CC Detecting abnormally low levels of DRM, or the nucleic acids, may be used
 CC to identify subjects with an increased risk of developing a
 CC hyperproliferative disease. Fragments of the nucleic acids are useful as
 CC probes and primers to detect or quantify drm and to screen genomic and
 CC cDNA libraries. Antibodies raised against DRM can be used to
 CC detect/quantify DRM in immunoassays. Fusion proteins of DRM and GFP are
 CC localised to the nucleus (in contrast cytoplasmic localisation of GFP

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CC itself) and so are more stable, e.g. on exposure to fixatives or
CC detergents, and thus form more versatile reagents, e.g. they can be used
CC in fluorescence-based assays that require cell fixation, or linked to
CC proteins or antibodies for use in enzyme-linked immunosorbent assays.
CC Stable EGFP can be attached to proteins during synthesis, allowing the
CC labeling of materials that are too unstable for chemical modification.
CC The present sequence represents a PCR primer for rat DRM
XX
SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 51 AGCCAGCGAA 60
Db 1 AGCCAGCGAA 10
|||||||
RESULT 239
AAZ99304
ID AAZ99304 standard; DNA; 10 BP.
XX
XX AAZ99304;
AC
XX
XX
XX 03-JUL-2000 (first entry)
XX
XX Probe used to obtain cancer associated gene cDNA sequences.
XX
XX Cancer associated gene; cancer specific gene; C1-9a11-2; CH8-2a13-1;
XX CH13-2a12-1; CH14-2a16-1; cancer; gene duplication; RNA overabundance;
XX breast cancer; lung cancer; glioblastoma; pancreatic cancer;
XX colon cancer; prostate cancer; hepatoma; myeloma; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200009655-A2.
PN
XX
XX 24-FEB-2000.
PD
XX
XX 10-AUG-1999; 99WO-US018101.
PP
XX
XX 10-AUG-1998; 98US-00132029.
PR
XX
XX (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.
PA
XX (USGO ) US GOVERNMENT.
PA
XX
XX Chen L;
PI
XX
XX WPI; 2000-224318/19.
XX
XX New cancer associated polypeptides, genes encoding them and antibodies
XX against them, useful for diagnosing breast cancer and screening for
XX anticancer drugs.
XX
XX Example 2; Page 87; 154pp; English.
XX
XX AAZ99299-299304 represent probes used to isolate cancer associated gene
XX cDNA sequences. These cancer specific genes are designated C1-9a11-2, CH8
XX -2a13-1, CH13-2a12-1, and CH14-2a16-1. These genes show RNA overabundance
XX in a majority of cancer cell lines tested, as well as a gene duplication
XX in many of the cancers. Probes and primers derived from the
XX polynucleotide sequence may be used to measure or detect altered gene
XX duplication or overabundance of RNA in cancerous cells. This allows the
XX screening of cancer, especially breast cancer, by correlating gene
XX duplication of RNA overexpression obtained in this method with an
XX increased risk for cancer. The polypeptide, and its antibodies, are used
XX as reagents for detecting altered protein expression in cancerous cells.
XX Both the cancer associated polypeptide and polynucleotide may be used to
XX screen for candidate drugs for cancer treatment. They are also used in
XX gene therapy to treat cancers such as lung cancer, glioblastoma,
XX pancreatic cancer, colon cancer, prostate cancer, hepatoma, myeloma and
XX breast cancer

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PT Isolated polynucleotides differentially expressed in antigen-presenting
 XX cells, useful in gene vaccines against cancer.
 PS Claim 1; Page 125; 130pp; English.
 XX
 CC Sequences AAZ77573-Z79709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC secretion of co-stimulatory signals, migration to T cell-rich sites,
 CC recruitment of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ACAAGAGCGC 13
 Db 1 ACAAGAGCGC 10
 RESULT 241
 AAZ50856
 ID AAZ50856 standard; DNA; 10 BP.
 XX
 AC AAZ50856;
 XX
 DT 31-MAY-2000 (first entry)
 XX
 DE Primer AP1 to identify tobacco salicylic acid inducible genes.
 XX
 KW Tobacco plant; salicylic acid inducible gene; fungal pathogen;
 KW SA-inducible gene; transgenic plant; pathogen resistance; PCR primer; ss.
 XX
 OS Nicotiana tabacum.
 XX
 FN WO200008186-A1.
 XX
 PD 17-FEB-2000.
 XX
 PF 02-AUG-1999; 99WO-EP005581.
 XX
 PR 03-AUG-1998; 98US-0095187P.
 XX
 PA (MOGE-) MOGEN INT NV.

XX Stuiiver MH, Jepson I, Horvath DM, Chua N;
 XX WPI; 2000-205725/18.
 DR
 XX Novel salicylic acid inducible genes from tobacco plants, useful for
 PT making transgenic plants with enhanced pathogenic resistance.
 XX
 PS Example 1; Page 51; 57pp; English.
 XX
 CC The patent discloses fifteen new salicylic acid (SA) inducible genes from
 CC Nicotiana tabacum, nine of which were subcloned and sequenced. Based on
 CC different kinetics of induction response, these genes were classified
 CC into four categories, class I, II, III and IV response genes. The SA-
 CC inducible genes are useful for making transgenic plants with enhanced
 CC pathogen resistance. The plants incorporating these genes show reduced
 CC susceptibility to fungal pathogens. The present sequence is an upstream
 CC primer AP1 used in differential display PCR reactions along with
 CC downstream primers T12MG or T12MC to identify tobacco SA-inducible genes
 XX
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 51 AGCCAGCGAA 60
 Db 1 AGCCAGCGAA 10
 RESULT 242
 AAZ48447
 ID AAZ48447 standard; DNA; 10 BP.
 XX
 AC AAZ48447;
 XX
 DT 27-MAR-2000 (first entry)
 XX
 DE Primer specific for C. jejuni.
 DE
 XX Microorganism; virus; polymerase chain reaction; food; cosmetic;
 KW clinical diagnostic; molecular beacon; PCR primer; ss.
 KW
 OS Campylobacter jejuni.
 XX
 FN WO9963112-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 18-MAY-1999; 99WO-US010940.
 XX
 PR 18-MAY-1998; 98US-0086025P.
 PR 17-MAY-1999; 99US-00086025.
 XX
 PA (HUNT-) HUNT WESSON INC.
 XX
 PI Romick TL, Fraser MS;
 XX WPI; 2000-086985/07.
 DR
 XX Detection of microorganisms and viruses, for use in the food and cosmetic
 PT industries and for clinical diagnostics.
 PT
 XX Disclosure; Page 25; 63pp; English.
 PS
 XX The invention provides a novel in vitro method for the detection of
 CC microorganisms and viruses. The method comprises: (1) forming a
 CC polymerase chain reaction (PCR) mixture by combining a predetermined
 CC volume of a sample to be tested for the presence of a nucleic acid
 CC sequence comprising 5'-TAGAAGC-3', known amounts of a first primer
 CC comprising 5'-GCTAAGGTCCAAAGT-3', and a second primer comprising 5'-
 CC AGAAGCGTCTCTCTACC-3', and PCR reagents; (2) forming a PCR product by

CC cycling the PCR mixture to amplify the nucleic acid sequence, if present,
 CC to replicate and attain 0.25-10000mg nucleotide product/mul mixture; (3)
 CC adding a probe containing DNA comprising 5'-GGTGGCTGCTTAAGCCACC-3', to
 CC the PCR mixture or to the PCR product to cause the DNA to hybridize with
 CC the nucleic acid sequence, if present, and change the conformation of the
 CC probe; and (4) determining whether or not bacteria are present in the
 CC sample by detecting the conformational change of the probe, a
 CC conformational change indicating the presence of bacteria in the sample.
 CC The methods can be used for the detection of viruses and microorganisms,
 CC including bacteria, yeast, molds and protista. They can be used in the
 CC food and cosmetic industry and in clinical diagnostics. Using the method
 CC it is not necessary to remove non-hybridized probe from the system
 XX
 SQ Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
 |||||
 Db 1 AGCCAGCGAA 10

RESULT 243
 AAA65614
 ID AAA65614 standard; DNA; 10 BP.

AC AAA65614;

XX 14-NOV-2000 (first entry)

XX Allograft inflammatory factor related PCR primer SEQ ID NO:28.

XX Allograft inflammatory factor 1; AIF-1; AIF-2; allograft gene; screening;
 KW diagnosis; allograft rejection; vascular inflammation; atherosclerosis;
 KW immunosuppressive; antiinflammatory; antiarteriosclerotic; PCR primer;
 XX ss.

OS Rattus sp.

PN US6077948-A.

XX 20-JUN-2000.

XX 21-DEC-1994; 94US-00361441.

XX 21-DEC-1993; 93US-00171385.

XX (HARD) HARVARD COLLEGE.

XX Utans U, Russell ME;

XX WPI; 2000-430614/37.

XX DNA encoding an allograft inflammatory factor-1, useful for diagnosing
 PT and treating allograft rejection and other conditions associated with
 PT vascular inflammation, especially atherosclerosis.

XX Example 1; Col 6; 59pp; English.

XX The present invention describes isolated DNA (I) encoding an allograft
 CC inflammatory factor-1 (AIF-1). AIF-1 has immunosuppressive,
 CC antiinflammatory and antiarteriosclerotic activities. AIF-1 is an
 CC inhibitor of expression of allograft factor such as Gal/GalNAc macrophage
 CC lectin. AIF-1 is useful for diagnosing and treating allograft rejection
 CC and other conditions associated to vascular inflammation, especially
 CC atherosclerosis. The present sequence represents a PCR primer which is
 CC used in an example from the present invention

XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 AGCCAGCGAA 60
 |||||
 Db 1 AGCCAGCGAA 10

RESULT 244
 AAH63382/C
 ID AAH63382 standard; cDNA; 10 BP.

XX AAH63382;

XX 20-SEP-2001 (first entry)

XX Human kidney specific transcriptome sequence SEQ ID NO: 222.

XX Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.

XX Homo sapiens.

XX WO200138577-A2.

XX 31-MAY-2001.

XX 21-NOV-2000; 2000WO-US031922.

XX 24-NOV-1999; 99US-00448480.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu VE, Vogelstein B, Kinzler KW;

XX WPI; 2001-367706/38.

XX New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcripts expressed in particular
 PT cell types.

XX Claim 11; Page 44; 94pp; English.

XX The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcripts described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcripts described in the exemplification of the invention

XX Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGGCTGGGG 19
 |||||
 Db 10 CGGCTGGGG 1

RESULT 245

AAF37532/C

ID AAF37532 standard; DNA; 10 BP.

XX AAF37532;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4271.

KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 DR
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 152; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle. The differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 3 C; 2 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 47 AAAGGCCGAG 56
 Db 10 AAAGGCCGAG 1
 |||||
 RESULT 246
 AAF37199/c
 ID AAF37199 standard; DNA; 10 BP.
 XX
 AC AAF37199;
 XX
 DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3938.
 DE
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 DR
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 PS Example; Page 140; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle. The differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 GGATACAACT 27
 Db 10 GGATACAACT 1
 |||||
 RESULT 247
 AAF36709/c
 ID AAF36709 standard; DNA; 10 BP.
 XX


```

RESULT 249
AAH77187
ID AAH77187 standard; DNA; 10 BP.
XX
AC AAH77187;
XX
XX 24-JAN-2002 (first entry)
XX
XX Rat arbitrary PCR primer AP-1.
XX
XX Rat; oestrogen agonist-inducible; hUO-44; cytostatic; ovary;
XX uterine cancer; ovarian cancer; uterine growth; uterine development;
XX ovarian growth; ovarian development; oestrogenic activity; PCR primer;
XX AP-1; ss.
XX
XX Rattus norvegicus.
XX
XX WO200175099-A1.
XX
XX 11-OCT-2001.
XX
XX 04-APR-2001; 2001WO-AU000379.
XX
XX 04-APR-2000; 2000US-0194566P.
XX
XX 15-AUG-2000; 2000AU-00009471.
XX
XX (NACA-) NAT CANCER CENT SINGAPORE PTE LTD.
XX (HUGH/) HUGHES E J L.
XX
XX Huynh TH;
XX
XX WPI; 2002-010789/01.
XX
XX Novel isolated UO-44 nucleic acid molecule useful for treating or
XX diagnosing uterine and/or ovarian cancers, comprises sequence
XX corresponding to uterine estrogen agonist-inducible genetic sequence in
XX mammal.
XX
XX Example 2; Page 37; 82pp; English.
XX
XX The sequence represents the rat arbitrary PCR primer AP-1, used in the
XX invention to amplify cDNA from rat ovary tissue. The invention relates to
XX a novel isolated UO-44 nucleic acid molecule comprising a sequence of
XX nucleotides corresponding to a uterine oestrogen agonist-inducible
XX genetic sequence in a mammal. The UO-44 sequences of the invention have
XX cytostatic activity. The UO-44 polynucleotide is useful in the
XX manufacture of a medicament for the treatment of a condition in a mammal,
XX for treating, diagnosing, detecting or monitoring uterine cancers and/or
XX ovarian cancers, and for producing the polypeptide. The polynucleotide or
XX polypeptide is useful for monitoring uterine and ovarian growth and
XX development and the level of oestrogenic activity in tissue including
XX cancer tissue. They are also useful for the generation of a range of
XX therapeutic molecules capable of modulating oestrogen agonist-mediated
XX cell growth and proliferation in the uterus including ovaries. The UO-44
XX polypeptide is useful to screen for naturally occurring antibodies to
XX itself
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 51 AGCCAGCGAA 60
XX Db 1 AGCCAGCGAA 10
XX
XX RESULT 250
AAH42350
ID AAL42350 standard; DNA; 10 BP.
XX
XX AAL42350;
XX
XX 28-JUN-2002 (first entry)
XX
XX Novel sand pear microsatellite DNA PCR primer 14.
XX
XX Sand pear; ss; PCR; primer; novel microsatellite DNA sequence;
XX Pyrus plant discrimination.
XX
XX Pyrus pyrifolia.
XX
XX JP2002034597-A.
XX
XX 05-FEB-2002.
XX
XX 21-JUL-2000; 2000JP-00220339.
XX
XX 21-JUL-2000; 2000JP-00220339.
XX
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX WPI; 2002-298819/34.
XX
XX A new microsatellite DNA derived from a Pyrus plant and discrimination of
XX Pyrus plants by using it.
XX
XX Example 1; Page 5; 22pp; Japanese.
XX
XX The invention comprises a novel microsatellite DNA sequence derived from
XX Pyrus plants. The invention also comprises a method for discriminating
XX Pyrus plants - utilising the novel Pyrus microsatellite DNA. The novel
XX microsatellite DNA sequence can be used in discriminating Pyrus plants.
XX The present DNA sequence represents a PCR primer specific for a novel
XX Pyrus pyrifolia (sand pear) microsatellite DNA sequence
XX
XX Sequence 10 BP; 4 A; 3 C; 3 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 51 AGCCAGCGAA 60
XX Db 1 AGCCAGCGAA 10
XX
XX RESULT 251
ACF12803
ID ACF12803 standard; DNA; 10 BP.
XX
XX ACF12803;
XX
XX 09-SEP-2003 (first entry)
XX
XX Primer used during DBPCR analysis #20.
XX
XX Endometrium; placenta; serine protease; gynecological; cytostatic;
XX cardiant; PRSP; infertility; endometriosis; cancer; pregnancy; primer;
XX PCR; ss.
XX
XX Synthetic.
XX
XX WO2003011905-A1.
XX
XX 13-FEB-2003.
XX
XX 30-JUL-2002; 2002WO-AU001010.
XX
XX 30-JUL-2001; 2001AU-00006707.
XX
XX (PRIN-) PRINCE HENRY'S INST MEDICAL RES.
XX

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RESULT 254
ADU18446/c
ID ADU18446 standard; DNA; 10 BP.
XX
AC ADU18446;
XX
DT 13-JAN-2005 (first entry)
XX
DE Hypoxia-related tumourigenesis-related SAGE tag #237.
XX
KW screening; hypoxia-related tumourigenesis;
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX
OS Unidentified.
XX
XX
XX
XX
XX WO2004092198-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US011087.
XX
XX 09-APR-2003; 2003US-0461712P.
XX
XX (GENZ ) GENZYME CORP.
XX
XX Nacht M;
XX
XX WPI; 2004-758333/74.
XX
XX Identifying agents that alter biological activity of a polypeptide
XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis
XX comprises contacting an agent with a target cell and monitoring activity
XX of expressed product.
XX
XX Disclosure; Page 97; 100pp; English.
XX
XX The invention comprises a method of screening for candidate agents
XX capable of altering the biological activity of a protein encoded by a
XX nucleotide involved in hypoxia-related tumorigenesis. The method of the
XX invention involves: contacting a test agent with a target cell expressing
XX the nucleotide, and monitoring the activity of the expressed protein
XX product; if the test agent modifies the activity of the expressed protein
XX then this is a candidate agent. The method of the invention is useful for
XX modifying hypoxia-induced gene regulation and for diagnosing, prognosing
XX or treating tumours. The present DNA sequence represents a SAGE tag that
XX was used in the exemplification of the invention.
XX
XX Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
XX
PS Disclosure; Page 61; 100pp; English.
XX
XX The invention comprises a method of screening for candidate agents
XX capable of altering the biological activity of a protein encoded by a
XX nucleotide involved in hypoxia-related tumorigenesis. The method of the
XX invention involves: contacting a test agent with a target cell expressing
XX the nucleotide, and monitoring the activity of the expressed protein
XX product; if the test agent modifies the activity of the expressed protein
XX then this is a candidate agent. The method of the invention is useful for
XX modifying hypoxia-induced gene regulation and for diagnosing, prognosing
XX or treating tumours. The present DNA sequence represents a SAGE tag that
XX was used in the exemplification of the invention.
XX
XX Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
XX
Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 21 TACAACCTCTG 30
Db 10 TACAACCTCTG 1
XX
RESULT 255
ADU18244/c
ID ADU18244 standard; DNA; 10 BP.
XX
AC ADU18244;
XX
DT 13-JAN-2005 (first entry)
XX
DE Hypoxia-related tumourigenesis-related SAGE tag #34.
XX
KW screening; hypoxia-related tumourigenesis;
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX
OS Unidentified.
XX
XX
XX WO2004092198-A2.
XX
XX 28-OCT-2004.
XX
XX 09-APR-2004; 2004WO-US011087.
XX
XX 09-APR-2003; 2003US-0461712P.
XX
XX (GENZ ) GENZYME CORP.
XX
XX Nacht M;
XX
XX WPI; 2004-758333/74.
XX
XX Identifying agents that alter biological activity of a polypeptide
XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis
XX comprises contacting an agent with a target cell and monitoring activity
XX of expressed product.
XX
XX Disclosure; Page 61; 100pp; English.
XX
XX The invention comprises a method of screening for candidate agents
XX capable of altering the biological activity of a protein encoded by a
XX nucleotide involved in hypoxia-related tumorigenesis. The method of the
XX invention involves: contacting a test agent with a target cell expressing
XX the nucleotide, and monitoring the activity of the expressed protein
XX product; if the test agent modifies the activity of the expressed protein
XX then this is a candidate agent. The method of the invention is useful for
XX modifying hypoxia-induced gene regulation and for diagnosing, prognosing
XX or treating tumours. The present DNA sequence represents a SAGE tag that
XX was used in the exemplification of the invention.
XX
XX Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;
XX
Query Match 13.0%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 21 TACAACCTCTG 30
Db 10 TACAACCTCTG 1
XX
RESULT 255
ADU20211/c
ID ADU20211 standard; DNA; 10 BP.
XX
AC ADU20211;
XX
DT 13-JAN-2005 (first entry)
XX
DE Hypoxia-related tumourigenesis-related SAGE tag #2002.
XX
KW screening; hypoxia-related tumourigenesis;
KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.
XX
OS Unidentified.
XX
XX

```

PT encoded by a polynucleotide involved in hypoxia-related tumorigenesis
 PT comprises contacting an agent with a target cell and monitoring activity
 PT of expressed product.

XX Disclosure; Page 56; 100pp; English.

XX The invention comprises a method of screening for candidate agents
 CC capable of altering the biological activity of a protein encoded by a
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the
 CC invention involves: contacting a test agent with a target cell expressing
 CC the nucleotide, and monitoring the activity of the expressed protein
 CC product; if the test agent modifies the activity of the expressed protein
 CC then this is a candidate agent. The method of the invention is useful for
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
 CC or treating tumours. The present DNA sequence represents a SAGE tag that
 CC was used in the exemplification of the invention.

XX Sequence 10 BP; 3 A; 1 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 TACAACCTCTG 30

Db 10 TACAACCTCTG 1

RESULT 257

AEC05483

ID AEC05483 standard; DNA; 11 BP.

XX AC AEC05483;

XX 20-OCT-2005 (first entry)

DE Factor VII mutant nucleic acid gene analysis probe, SEQ ID 2.

XX analysis; SNP detection; factor VII; probe; ss.

XX Synthetic.

XX JP2005218310-A.

XX 18-AUG-2005.

XX 03-FEB-2004; 2004JP-00026821.

XX 03-FEB-2004; 2004JP-00026821.

XX (DOKU-) DOKURITSU GYOSHI HOJIN BUSSHITSU ZAIRYO.

XX Miyahara Y, Sakata T;

XX WPI; 2005-575324/59.

XX Device for gene analysis e.g. gene polymorphism analysis, comprises
 PT insulation film substance immobilized with nucleic acid probe specific
 PT for target, semiconductor substrate and reference electrode.

XX Example 1; SEQ ID NO 2; 22pp; Japanese.

XX The invention relates to a novel device for gene analysis. The device
 CC comprises an insulation film substance, a semiconductor substrate and a
 CC reference electrode. The insulation film substance is immobilized on one
 CC side with a nucleic acid probe and contacted with a sample solution
 CC comprising a target gene, and the other side of the surface of insulation
 CC film substance is contacted with the semiconductor substrate, and the
 CC reference electrode is in the sample solution. The novel device is
 CC preferably useful for analyzing a gene polymorphism. The device enables
 CC rapid, cost effective, highly sensitive and accurate gene analysis. This
 CC oligo represents a factor VII mutant nucleic acid probe used in the gene
 CC analysis of the invention.

XX Sequence 11 BP; 1 A; 4 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 GTCCTCTGAG 42

Db 2 GTCCTCTGAG 11

RESULT 258

AAQ24028/C

ID AAQ24028 standard; DNA; 12 BP.

XX AC AAQ24028;

XX 25-MAR-2003 (revised)

DT 21-SEP-1992 (first entry)

XX Herpesvirus inhibiting antisense oligonucleotide.

XX HSV; treatment; diagnosis; HSV-1; HSV-2; varicella zoster;

XX Epstein-Barr virus; cytomegalovirus; CMV; HIV; AIDS.

XX Synthetic.

XX WO9205284-A.

XX 02-APR-1992.

XX 18-SEP-1991; 91WO-US006646.

XX 21-SEP-1990; 90US-00586185.

XX (UYMA-) UNIV MARYLAND BALTIMORE.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Aurelian L, Tso P;

XX WPI; 1992-132145/16.

XX New anti-sense oligo:nucleotide(s) for inhibiting HSV - also used for
 PT diagnosis and for inhibiting HIV activation by herpes virus.

XX Claim 1; Page 38; 77pp; English.

XX The sequence is that of an antisense oligonucleotide which can be used
 CC for inhibiting growth or replication of herpesviruses. It corresponds to
 CC an antisense sequence of a herpesvirus site, pref. in a gene that is
 CC essential for synthesising nucleic acids e.g. the immediate early genes
 CC or Vmw65. It can be prepd. by solid phase triester or phosphor- amidite
 CC chemistry or by recombinant DNA techniques. It can be used for treating
 CC infection by herpesviruses, e.g. herpes simplex type 1 (HSV-1) and type 2
 CC (HSV-2), varicella zoster (VSV), Epstein-Barr (EBV), cytomegalovirus
 CC (CMV), human herpesvirus 6 (HHV-6) and 7 (HHV-7). In addition, the
 CC inhibition of herpesvirus growth or replication may indirectly forestall
 CC the progression of events from HIV exposure to the clinical manifestation
 CC of AIDS. It may also be useful in the detection, diagnosis and
 CC manipulation of herpes virus. See also AAQ23764-Q23788 and AAQ24014-
 CC Q24044. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 12 BP; 3 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GAGTCTCTCTG 40

Db 12 GAGTCTCTCTG 3

```

RESULT 259
ABH77995
ID ABH77995 standard; DNA; 12 BP.
XX AC ABH77995;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 277988 for detecting SNP TSC0005414.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 277988; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT99989
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 20 ATCAACTCT 29
XX Db 1 ATCAACTCT 10
XX
XX RESULT 260
ABT41039
ID ABT41039 standard; DNA; 12 BP.
XX AC ABT41039;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 341012 for detecting SNP TSC0041801.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 277988; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT99989
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 5 A; 3 C; 0 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 20 ATCAACTCT 29
XX Db 1 ATCAACTCT 10
XX
XX RESULT 261
ABI67527/c
ID ABI67527 standard; DNA; 12 BP.
XX AC ABI67527;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 367500 for detecting SNP TSC0056379.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.

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KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX XX WPI; 2001-657177/75.
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX Claim 1; SEQ ID NO 341012; 29pp + Sequence Listing; German.
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC99989, ABP00010-ABF99989, ABH00010-ABH99989 and ABT00010-ABT99989
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 12 BP; 6 A; 3 C; 0 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 13.0%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 20 ATCAACTCT 29
XX Db 1 ATCAACTCT 10
XX
XX RESULT 261
ABI67527/c
ID ABI67527 standard; DNA; 12 BP.
XX AC ABI67527;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 367500 for detecting SNP TSC0056379.
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPIG-) EPIGENOMICS AG.

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Query Match      13.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GAGGTAAGA 51
Db 10 GAGGTAAGA 1

RESULT 264
ABI53146/C
ID ABI53146 standard; DNA; 12 BP.
XX AC
XX AC ABI53146;
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 353119 for detecting SNP TSC0010241.
XX KW
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.
XX PD
XX PD 18-OCT-2001.
XX PF
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR
XX PR 07-APR-2000; 2000DE-01019173.
XX PA
XX PA (EPIG-) EPIGENOMICS AG.
XX PI
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 353119; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 4 A; 0 C; 3 G; 5 T; 0 U; 0 Other;

Query Match      13.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATCAACTCT 29
Db 11 ATCAACTCT 2

RESULT 265
ABH81026
ID ABH81026 standard; DNA; 12 BP.
XX XX

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AC ABH81026;
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 281019 for detecting SNP TSC0009317.
XX KW
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.
XX PD
XX PD 18-OCT-2001.
XX PF
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR
XX PR 07-APR-2000; 2000DE-01019173.
XX PA
XX PA (EPIG-) EPIGENOMICS AG.
XX PI
XX PI Olek A, Piepenbrock C, Berlin K;
XX PI WPI; 2001-657177/75.
XX DR
XX DR Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PT designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX XX
XX PS Claim 1; SEQ ID NO 281019; 29pp + Sequence Listing; German.
XX CC
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX XX
XX SQ Sequence 12 BP; 7 A; 0 C; 4 G; 1 T; 0 U; 0 Other;

Query Match      13.0%; Score 10; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GAGGTAAGA 51
Db 1 GAGGTAAGA 10

RESULT 266
ABH91914/C
ID ABH91914 standard; DNA; 12 BP.
XX AC
XX AC ABH91914;
XX DT
XX DT 22-FEB-2002 (first entry)
XX DE
XX DE Oligonucleotide primer SEQ ID NO 291907 for detecting SNP TSC0014997.
XX KW
XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200177384-A2.

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XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DB-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PF designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 291907; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX Query Match 13.0%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GAGGTAAGA 51
DB 10 GAGGTAAGA 1
|||||||

RESULT 267
ABH78388
ID ABH78388 standard; DNA; 12 BP.
XX AC ABH78388;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 278381 for detecting SNP TSC0005966.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DB-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PF designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 278381; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010
XX CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
XX CC represent the oligomers described in the invention. NOTE: The sequence
XX CC data for this patent did not form part of the printed specification, but
XX CC was obtained in electronic format from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 12 BP; 3 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
XX Query Match 13.0%; Score 10; DB 1; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AGGTAAGAG 52
DB 2 AGGTAAGAG 11
|||||||

RESULT 268
ABI47414
ID ABI47414 standard; DNA; 12 BP.
XX AC ABI47414;
XX DT 22-FEB-2002 (first entry)
XX DE Oligonucleotide primer SEQ ID NO 347387 for detecting SNP TSC0045063.
XX SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX PN WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-IB000713.
XX PR 07-APR-2000; 2000DB-01019173.
XX PA (EPIG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX PF designed to detect single-nucleotide polymorphisms and cytosine
XX PT methylation status.
XX PS Claim 1; SEQ ID NO 347387; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
XX CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX CC and cytosine methylation status in chemically pretreated genomic DNA. The
XX CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX CC range of diseases including immune system, gastrointestinal, respiratory,
XX CC central nervous system, cardiovascular and metabolic disorders. The
XX CC oligomers are also used for detecting cell type differentiation. ABC00010

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CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 5 A; 0 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match      13.0%; Score 10; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 AGGTAAGAG 52
Db 3 AGGTAAGAG 12
|||||
|||||

RESULT 269
ABI22756/c
ID ABI22756 standard; DNA; 12 BP.
XX
AC ABI22756;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 322729 for detecting SNP TSC0031029.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 322729; 29pp + Sequence Listing; German.
XX
SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 0 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match      13.0%; Score 10; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATACAACCTCT 29
Db 1 ATACAACCTCT 29
|||||
|||||

RESULT 271
ABI24690/c
ID ABI24690 standard; DNA; 12 BP.
XX
AC ABI24690;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 324663 for detecting SNP TSC0032163.

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Db 11 ATACAACCTCT 2
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|||||

RESULT 270
ABI66720
ID ABI66720 standard; DNA; 12 BP.
XX
AC ABI66720;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 366693 for detecting SNP TSC0055920.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
PI WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 366693; 29pp + Sequence Listing; German.
XX
SQ This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 12 BP; 4 A; 4 C; 0 G; 4 T; 0 U; 0 Other;

  Query Match      13.0%; Score 10; DB 1; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.3e+02;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ATACAACCTCT 29
Db 1 ATACAACCTCT 10
|||||
|||||

RESULT 271
ABI24690/c
ID ABI24690 standard; DNA; 12 BP.
XX
AC ABI24690;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide primer SEQ ID NO 324663 for detecting SNP TSC0032163.

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XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 324663; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 ATCAACTCT 29
 DB 12 ATCAACTCT 3
 RESULT 272
 ABC48256/C
 ID ABC48256 standard; DNA; 13 BP.
 XX AC ABC48256;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 48273 for detecting SNP TSC0013776.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 48273; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 12 BP; 5 A; 0 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 ATCAACTCT 29
 DB 12 ATCAACTCT 3
 RESULT 272
 ABC48256/C
 ID ABC48256 standard; DNA; 13 BP.
 XX AC ABC48256;
 XX 21-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 48273 for detecting SNP TSC0013776.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 48273; 29pp + Sequence Listing; German.

PR 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 48273; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 3 A; 0 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 ATCAACTCT 29
 DB 10 ATCAACTCT 1
 RESULT 273
 ABC04048
 ID ABC04048 standard; DNA; 13 BP.
 XX AC ABC04048;
 XX 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 4039 for detecting SNP TSC0001514.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX Claim 1; SEQ ID NO 4039; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42 GAGGTAAGA 51
DB 2 GAGGTAAGA 11
|||||
RESULT 274
ABF37938
ID ABF37938 standard; DNA; 13 BP.
XX
AC ABF37938;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 137935 for detecting SNP TSC0034489.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 137935; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42 GAGGTAAGA 51
DB 1 GAGGTAAGA 10
|||||
RESULT 275
ABC48257
ID ABC48257 standard; DNA; 13 BP.
XX
AC ABC48257;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 48274 for detecting SNP TSC0013776.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
FN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 48274; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 4 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 ATCAACTCT 29
DB 4 ATCAACTCT 13
|||||
RESULT 276

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ABC62658
ID ABC62658 standard; DNA; 13 BP.
XX
AC ABC62658;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 62675 for detecting SNP TSC0016605.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 62675; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 6 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
XX
Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGAGGTTAAAG 50
Db 3 AGAGGTTAAAG 12
|||||
3 AGAGGTTAAAG 12

RESULT 277
ABF37939/c
ID ABF37939 standard; DNA; 13 BP.
XX
AC ABF37939;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 137936 for detecting SNP TSC0034489.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

Homo sapiens.
WO200177384-A2.
18-OCT-2001.
06-APR-2001; 2001WO-IB000713.
07-APR-2000; 2000DE-01019173.
(EPIG-) EPIGENOMICS AG.
Olek A, Piepenbrock C, Berlin K;
WPI; 2001-657177/75.
Set of oligonucleotides, useful for diagnosis and cell typing, is
designed to detect single-nucleotide polymorphisms and cytosine
methylation status.
Claim 1; SEQ ID NO 137936; 29pp + Sequence Listing; German.
This invention describes novel oligonucleotide primers or peptide nucleic
acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
and cytosine methylation status in chemically pretreated genomic DNA. The
oligonucleotides are used for diagnosis and/or prognosis of cancer and a
range of diseases including immune system, gastrointestinal, respiratory,
central nervous system, cardiovascular and metabolic disorders. The
oligomers are also used for detecting cell type differentiation. ABC00010
-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
represent the oligomers described in the invention. NOTE: The sequence
data for this patent did not form part of the printed specification, but
was obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences
Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
Query Match 13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 GAGGTTAAGA 51
Db 13 GAGGTTAAGA 4
|||||
13 GAGGTTAAGA 4

RESULT 278
ABF82004
ID ABF82004 standard; DNA; 13 BP.
XX
AC ABF82004;
XX
DT 22-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 182001 for detecting SNP TSC0044987.
XX
KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; human; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;

```

XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 182001; 29pp + Sequence Listing; German.
 CC
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 1 C; 4 G; 2 T; 0 U; 0 Other;
 CC
 CC Query Match 13.0%; Score 10; DB 1; Length 13;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 40 GAGAGGTAA 49
 DB 3 GAGAGGTAA 12
 RESULT 279
 ABH65593
 ID ABH65593 standard; DNA; 13 BP.
 XX
 AC ABH65593;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 265570 for detecting SNP TSC0064365.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 OS WPI; 2001-657177/75.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 OS WPI; 2001-657177/75.
 XX
 DE Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 265570; 29pp + Sequence Listing; German.
 CC
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 6 A; 1 C; 4 G; 2 T; 0 U; 0 Other;

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 5 A; 4 C; 0 G; 3 T; 0 U; 1 Other;
 CC
 CC Query Match 13.0%; Score 10; DB 1; Length 13;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 20 ATACAACTCT 29
 DB 3 ATACAACTCT 12
 RESULT 280
 ABC62659/C
 ID ABC62659 standard; DNA; 13 BP.
 XX
 AC ABC62659;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 62676 for detecting SNP TSC0016605.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 OS WPI; 2001-657177/75.
 XX
 PN Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 62676; 29pp + Sequence Listing; German.
 CC
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 6 C; 0 G; 6 T; 0 U; 0 Other;
 CC
 CC Query Match 13.0%; Score 10; DB 1; Length 13;
 CC Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 AGAGGTTAAAG 50
 Db 11 AGAGGTTAAAG 2
 |||||
 |||||

RESULT 281
 ABH24089/C
 ID ABH24089 standard; DNA; 13 BP.
 XX AC ABH24089;
 XX DT 22-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 224066 for detecting SNP TSC0054592.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX DT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PF Claim 1; SEQ ID NO 224066; 29pp + Sequence Listing; German.
 XX PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 3 A; 5 C; 0 G; 4 T; 0 U; 1 Other;
 Query Match 13.0%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAA 48
 Db 11 TGAGAGGTAA 2
 |||||
 |||||

RESULT 282
 ABC04049/C
 ID ABC04049 standard; DNA; 13 BP.
 XX AC ABC04049;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 74402 for detecting SNP TSC0019120.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.

DT 20-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 4040 for detecting SNP TSC0001514.
 DE SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.
 XX PF 06-APR-2001; 2001WO-IB000713.
 XX PR 07-APR-2000; 2000DE-01019173.
 XX PA (EPIG-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX DR WPI; 2001-657177/75.
 XX DT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX PF Claim 1; SEQ ID NO 4040; 29pp + Sequence Listing; German.
 XX PS This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 13 BP; 4 A; 4 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 GAGGTTAAAGA 51
 Db 12 GAGGTTAAAGA 3
 |||||
 |||||

RESULT 283
 ABC74385/C
 ID ABC74385 standard; DNA; 13 BP.
 XX AC ABC74385;
 XX DT 21-FEB-2002 (first entry)
 XX DE Oligonucleotide SEQ ID NO 74402 for detecting SNP TSC0019120.
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 XX KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; se;
 XX KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX PN WO200177384-A2.
 XX PD 18-OCT-2001.

XX 06-APR-2001; 2001WO-IB000713.
 PF
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 74402; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 3 A; 5 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 39 TGAGAGGTAA 48
 Db 10 TGAGAGGTAA 1
 |||||
 |||||
 RESULT 284
 ABH24088
 ID ABH24088 standard; DNA; 13 BP.
 XX
 AC ABH24088;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX Oligonucleotide SEQ ID NO 224065 for detecting SNP TSC0054592.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX

PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 224065; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 4 A; 0 C; 5 G; 3 T; 0 U; 1 Other;
 Query Match 13.0%; Score 10; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 39 TGAGAGGTAA 48
 Db 3 TGAGAGGTAA 12
 |||||
 |||||
 RESULT 285
 ABC74384
 ID ABC74384 standard; DNA; 13 BP.
 XX
 AC ABC74384;
 XX
 XX 21-FEB-2002 (first entry)
 DT
 XX Oligonucleotide SEQ ID NO 74401 for detecting SNP TSC0019120.
 DE
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX Homo sapiens.
 OS
 XX WO200177384-A2.
 PN
 XX 18-OCT-2001.
 PD
 XX 06-APR-2001; 2001WO-IB000713.
 PF
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 74401; 29pp + Sequence Listing; German.
 PS
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABT00010-ABT2073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

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CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 39 TGAGAGGTAA 48
Db 4 TGAGAGGTAA 13

RESULT 286
ABH65592/c
ID ABH65592 standard; DNA; 13 BP.
XX
XX AC ABH65592;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 265569 for detecting SNP TSC0064365.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DB-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 265569; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 3 A; 0 C; 4 G; 5 T; 0 U; 1 Other;

Query Match      13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 ATACAACCTCT 29
Db 11 ATACAACCTCT 2

RESULT 287
ABF82005/c
ID ABF82005 standard; DNA; 13 BP.
XX
XX AC ABF82005;
XX
XX 22-FEB-2002 (first entry)
XX
XX Oligonucleotide SEQ ID NO 182002 for detecting SNP TSC0044987.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DB-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
XX Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single-nucleotide polymorphisms and cytosine
XX methylation status.
XX
XX Claim 1; SEQ ID NO 182002; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation. ABC00010
XX -ABC9989, ABF00010-ABF9989, ABH00010-ABH9989 and ABI00010-ABI82073
XX represent the oligomers described in the invention. NOTE: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 13 BP; 2 A; 4 C; 1 G; 6 T; 0 U; 0 Other;

Query Match      13.0%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 GAGAGGTAAA 49
Db 11 GAGAGGTAAA 2

RESULT 288
ADQ58875/c
ID ADQ58875 standard; DNA; 13 BP.
XX
XX AC ADQ58875;
XX
XX 23-SEP-2004 (first entry)
XX
XX Yin yang-1 potential splice variant acceptor site #5.
XX
XX antidiabetic; immunosuppressive; cytostatic; Yin Yang-1;

```

KW transcription factor; type 1 diabetes; transgenic; diabetes;
 KW multifunctional transcription factor; type 2 diabetes;
 KW autoimmune disease; cancer; mineral metabolism disorder;
 KW lipid metabolism disorder; rat; YY-1; splice variant; acceptor site; ds.
 OS Rattus norvegicus.
 XX
 XX WO2004056857-A2.
 XX
 XX 08-JUL-2004.
 XX
 XX 19-DEC-2003; 2003WO-EP014762.
 XX
 XX 20-DEC-2002; 2002DE-01061650.
 XX
 XX (UYGR) UNIV GREIFSWALD.
 XX
 XX Kloeting I, Kloeting N;
 XX
 XX WPI; 2004-507695/48.
 XX
 XX New variant of the Yin Yang-1 transcription factor, useful for treating
 PT e.g. diabetes and autoimmune disease, also for diagnosing predisposition
 PT and in screening for therapeutic agents.
 XX
 XX Disclosure; Page 62; 193pp; German.
 XX
 CC The invention describes a protein variant of the Yin Yang-1 transcription
 CC factor (I), having a 411 amino acid (aa) sequence (4) reproduced. Also
 CC described are: protein (Ia) that is a homologue of (4) and includes Arg a
 CC position 303 and Lys at position 311; peptide (II) that is a fragment of
 CC (I) or (Ia) and includes the positions 303 and 311 of (4); nucleic acid
 CC (III) that encodes (I), (Ia) or (II); an antibody (Ab) directed against
 CC (I) or (Ia); methods for determining a tendency to develop type 1
 CC diabetes; transgenic non-human mammal (A) in which the germ and somatic
 CC cells contain a nucleic acid (or segment) encoding a 411 aa sequence (2),
 CC or sequences with at least 95, best 99% homology, where the homologue
 CC includes 303Met and 311Arg; and use of (A) to screen for compounds (B)
 CC that are protective against diabetes. The methods are useful for
 CC modulating activity of the Y1 (Yin Yang-1) multifunctional transcription
 CC factor. (I), or its homologues and peptides, also nucleic acids encoding
 CC them and antisense oligonucleotides, are useful for treatment of type 1
 CC and 2 diabetes, autoimmune diseases, cancer and disorders of mineral and
 CC lipid metabolism. Detecting mutations in the human analogue of (4) is
 CC used to determine a predisposition for these diseases. Transgenic animals
 CC that contain the sequence encoding (4), or its homologues, are used to
 CC screen for agents protective against diabetes. This sequence represents a
 CC potential splice acceptor site for splice variants of Yin yang-1
 CC transcription factor.
 XX
 XX Sequence 13 BP; 3 A; 7 C; 1 G; 2 T; 0 U; 0 Other;
 QY Query Match 13.0%; Score 10; DB 1; Length 13;
 DB Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 TCTGAGAGGT 46
 DB 10 TCTGAGAGGT 1
 RESULT 289
 AAT10984/C
 ID AAT10984 standard; DNA; 14 BP.
 XX
 XX AAT10984;
 XX
 XX 25-MAR-2003 (revised)
 DT 19-JUN-1996 (first entry)
 XX
 XX H.influenzae detection probe binds to 16S rRNA gene at pos. 1255-69.
 DE
 XX Probe; Haemophilus influenzae; 16S rRNA gene; E.coli; helper probe;
 KW

KW acridinium ester label; H.aphrophilus; H.ducrei; H.haemolyticus;
 KW H.parahaemolyticus; H.parainfluenzae; H.paraphrophilus; ss.
 XX
 OS Synthetic.
 XX
 XX US5472843-A.
 PN
 XX 05-DEC-1995.
 XX
 XX 01-APR-1994; 94US-00221968.
 XX
 XX 25-APR-1991; 91US-00690788.
 PR
 XX (GENP-) GEN-PROBE INC.
 PA
 XX Milliman CL;
 PI
 XX WPI; 1996-029808/03.
 DR
 XX
 XX Detection of Haemophilus influenzae nucleic acid - using new
 PT oligo:nucleotide probes.
 PT
 XX Example 1; Col 9; 9pp; English.
 PS
 XX
 XX Probes AAT10983-4 are used for the specific detection of Haemophilus
 CC influenzae. They bind to a region of the H.influenzae 16S rRNA gene at a
 CC pos. corresp. to bases 837-854 or 1255-69 of the E.coli 16S rRNA gene.
 CC The probes can also be used in the detection by the helper probes
 CC AAT10985-9. The probes are pref. labelled with an acridinium ester label.
 CC The probes are specific for H.influenzae and do not bind to nucleic acids
 CC from H.aphrophilus, H.ducrei, H.haemolyticus, H.parahaemolyticus,
 CC H.parainfluenzae or H.paraphrophilus. (Updated on 25-MAR-2003 to correct
 CC PF field.)
 XX
 XX Sequence 14 BP; 1 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
 SQ
 QY Query Match 13.0%; Score 10; DB 1; Length 14;
 DB Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 55 AGCGAAGCTG 64
 DB 12 AGCGAAGCTG 3
 RESULT 290
 AAV99057/C
 ID AAV99057 standard; RNA; 14 BP.
 XX
 XX AAV99057;
 XX
 XX 17-MAR-1999 (first entry)
 DT
 XX
 XX Human EGF-R target sequence nucleotide position 3489.
 DE
 XX
 XX Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
 KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
 KW cancer; genetic drift; detection; mutation; ss.
 XX
 XX Homo sapiens.
 OS
 XX WO9833893-A2.
 PN
 XX 06-AUG-1998.
 PD
 XX
 XX 14-JAN-1998; 98WO-US000730.
 XX
 XX 31-JAN-1997; 97US-0036476P.
 PR
 XX 04-DEC-1997; 97US-00985162.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX (UYAS-) UNIV ASTON.
 XX

PI Akhtar S, Fell P, Mcswiggen JA;
 DR WPI, 1998-437449/37.
 XX
 XX Enzymatic nucleic acids - which cleave RNA derived from an epidermal
 PT growth factor receptor, useful for inhibiting cell proliferation and for
 PT treating cancers.
 XX
 PS Claim 6; Page 89; 109pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules (NAMS)
 CC which specifically cleave RNA derived from an epidermal growth factor
 CC receptor (EGF-R) gene. AA97221 to AA98043 and AA98979 to AA99090
 CC represent specifically claimed target sequence from human EGF-R. AA98044
 CC to AA98866 and AA98867 to 98878 represent hammerhead ribozymes and
 CC hairpin ribozymes respectively for human EGF-R. The NAMS are useful for
 CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
 CC expression levels e.g. to inhibit cell proliferation in the prevention or
 CC treatment of cancers. The NAMS can also be used as diagnostic tools to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of EGF-R RNA in a cell
 XX
 SQ Sequence 14 BP; 0 A; 6 C; 5 G; 0 T; 3 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 49 AGAGCCAGCG 58
 DB 14 AGAGCCAGCG 5
 RESULT 291
 AA67150/c
 ID AA67150 standard; DNA; 14 BP.
 XX
 AC AA67150;
 DT 11-JAN-1999 (first entry)
 XX
 DE Haemophilus influenzae 16S rRNA probe #1.
 XX
 KW Haemophilus influenzae; 16S rRNA; probe; hybridisation; identification;
 KW bacterial colony; ribosomal RNA; ss.
 XX
 OS Synthetic.
 OS Haemophilus influenzae.
 XX
 PN US5830654-A.
 XX
 PD 03-NOV-1998.
 XX
 PF 04-DEC-1995; 95US-00567196.
 XX
 PR 25-APR-1991; 91US-00690788.
 PR 01-APR-1994; 94US-00221968.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Millman CL;
 XX
 DR WPI, 1998-609234/51.
 XX
 PT Nucleic acid hybridisation probe specific for Haemophilus influenzae -
 PT useful for identification of H. influenzae, optionally used with helper
 PT probes.
 XX
 PS Claim 1; Col 13; 10pp; English.
 XX
 CC The present sequence represents a nucleic acid hybridisation probe that
 CC hybridises to Haemophilus influenzae rRNA in a region corresponding to
 CC nucleotides 1255-1268 of E. coli 16S rRNA. The probe can be labelled,

CC especially with an acridinium ester, and used in an assay for H.
 CC influenzae, optionally together one or more helper probes. The probe does
 CC not hybridise to nucleic acids from H. aphrophilus, H. ducreyi, H.
 CC haemolyticus, H. parahaemolyticus, H. parainfluenzae or H.
 CC paraaphrophilus. The probe enables rapid, non-subjective identification
 CC of the presence of specific ribosomal RNA sequences that are unique to
 CC all serotypes and bio-types of H. influenzae
 XX
 SQ Sequence 14 BP; 1 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
 Query Match 13.0%; Score 10; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 55 AGCGAAGCTG 64
 DB 12 AGCGAAGCTG 3
 RESULT 292
 AAA17665/c
 ID AAA17665 standard; RNA; 14 BP.
 XX
 AC AAA17665;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Aryl hydrocarbon nuclear transport target site SEQ ID NO:891.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US006507.
 XX
 PR 27-MAR-1998; 98US-0079678P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX
 DR WPI, 1999-591315/50.
 XX
 PT Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 PS Claim 53; Page 90; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence

CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA24222 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (AMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 14 BP; 3 A; 5 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 13.0%; Score 10; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 GAAGCTGATG 67
 |||||
 Db 10 GAAGCTGATG 1

RESULT 293
 AAN92945/c
 ID AAN92945 standard; DNA; 12 BP.
 XX
 AC AAN92945;
 XX
 DT 01-JUL-1990 (first entry)
 XX
 DE Consensus sequence for mammalian expression vector.
 XX
 KW Murine autonomously replicating sequence; consensus sequence;
 KW mammalian expression vector.
 XX
 OS Mouse.
 XX
 PN EP306848-A.
 XX
 PD 15-MAR-1989.
 XX
 PF 02-SEP-1988; 88EP-00114317.
 XX
 PR 09-SEP-1987; 87DE-03730246.
 XX
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Grummt F, Weidle U;
 XX
 XX WPI; 1989-078357/11.
 DR

XX Expression vectors for mammalian cells - with two consensus sequences and
 XX inefficient selection system.
 PT
 PT Claim 2; Page 8; 12pp; German.
 PS
 XX

XX The inventors claim vectors for the expression of heterologous proteins
 CC in mammalian cells. Each vector has a first and second consensus sequence
 CC (CS). The CS or their homologues are present in known murine autonomously
 CC replicating sequences (MuARS). The first CS is homologous to AAN92945.
 CC The inefficient selection system comprises the tk gene and a truncated tk
 CC promoter. The vectors also contain a gene coding for a protein and the
 CC necessary promoter and terminator sequences for the expression of this
 CC gene. The expression vectors provide rapid amplification, allow selection
 CC of best clones in a short time, are of universal utility in mammalian
 CC cells, and are free of viral origin sequences
 XX

SQ Sequence 12 BP; 4 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 12.2%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 1.6e+02;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 34 TCCTCTGAGAG 44
 |||||
 Db 11 TCCTCTGAGAG 1
 RESULT 294
 ACC46925
 ID ACC46925 standard; DNA; 20 BP.
 XX
 AC ACC46925;
 XX
 DT 05-JUN-2003 (first entry)
 XX
 DE Human phospholipase A2 antisense oligonucleotide SEQ ID NO:22.
 XX
 KW Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;
 KW phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;
 KW antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;
 KW psoriasis; diabetes; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 XX
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyl (2'-MOE) gapmer"
 XX
 XX WO200297133-A1.
 PN
 XX
 XX 05-DEC-2002.
 PD
 XX
 XX 21-MAY-2002; 2002WO-US016135.
 PF
 XX
 XX 25-MAY-2001; 2001US-00865866.
 PR
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX
 XX Bennett CF, Wyatt JR;
 XX
 XX WPI; 2003-140495/13.
 DR
 XX
 XX New compound that hybridizes with and inhibits the expression of
 PT Phospholipase A2, group IIA, useful for preparing a composition for
 PT treating or preventing inflammation, cancer, psoriasis or diabetes.
 PT
 XX
 XX Claim 3; Page 86; 135pp; English.
 PS
 XX
 XX The present invention describes a compound (I) comprising 8-50
 CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,
 CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase
 CC A2, group IIA (synovial), where the compound specifically hybridizes with
 CC and inhibits the expression of phospholipase A2, group IIA (synovial).
 CC Also described: (1) a composition comprising the compound and a carrier
 CC or diluent; (2) a method of inhibiting the expression of phospholipase
 CC A2, group IIA in cells or tissues; and (3) a method of treating an animal
 CC having a disease or condition associated with phospholipase A2, group IIA
 CC (synovial). (I) has antiinflammatory, antidiabetic, cytostatic and
 CC antipsoriatic activities, and can be used in vaccines and in gene
 CC therapy. The compound (I) can be used for preparing a composition for
 CC treating or preventing inflammation, cancer, psoriasis or diabetes. The
 CC present sequence represents a human phospholipase A2 group IIA (synovial)

CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
 CC example from the present invention
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 3 G; 6 T; 0 U; 0 Other;
 Query Match 12.2%; Score 9.4; DB 1; Length 20;
 Best Local Similarity 90.9%; Pred. No. 2.4e+02;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 35 CCTCTGAGAGG 45
 Db 8 CCTCTGAGAGG 18
 |||||
 |||||

RESULT 295
 ID AAZ64698 standard; RNA; 14 BP.
 XX
 AC AAZ64698;
 XX
 DT 28-MAR-2000 (first entry)
 XX
 DE Substrate for hairpin ribozyme which cleaves HCV at nt. 886.
 XX
 KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
 KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
 KW autoimmune disease; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO9955847-A2.
 XX
 PD 04-NOV-1999.
 XX
 XX 26-APR-1999; 99WO-US009027.
 XX
 XX 27-APR-1998; 98US-0083217P.
 PR 18-SEP-1998; 98US-0100842P.
 PR 25-FEB-1999; 99US-00257608.
 PR 23-MAR-1999; 99US-00274553.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Meswigen JA, Roberts B, Pavco PA, Macejak D;
 XX
 DR WPI; 2000-062023/05.
 XX
 PT Novel ribozymes for the treatment of diseases and conditions related to
 PT hepatitis C infection.
 XX
 PS Claim 2; Page 94; 123pp; English.
 XX
 CC The present sequence represents the preferred target sequence of an
 CC enzymatic nucleic acid, especially a hairpin ribozyme, which cleaves the
 CC Hepatitis C virus (HCV) RNA sequence at the base position given in the
 CC descriptor line. The HCV sequence was screened for optimal ribozyme
 CC target sites using a computer folding algorithm and regions of the mRNA
 CC which did not form secondary folding structures and contained potential
 CC ribozyme cleavage sites were identified. Ribozymes were synthesised to
 CC target these sites and their activities optimised by either varying the
 CC length of the binding arms or by modification to prevent degradation by
 CC nucleases. The ribozymes of the invention inhibit gene expression and/or
 CC viral replication, and are used to treat diseases associated with
 CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
 CC hepatocellular carcinoma. The ribozymes may be used in combination with
 CC interferon to treat HCV infection, other infectious diseases, autoimmune
 CC diseases, and cancer
 XX
 SQ Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
 Query Match 11.4%; Score 8.8; DB 1; Length 14;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAACAGACGGC 13
 |||||
 Db 14 AAACAGACGGC 3
 |||||

RESULT 296
 ABX01535/c
 ID ABX01535 standard; RNA; 14 BP.
 XX
 AC ABX01535;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE Hepatitis C virus substrate #20 for HCV hairpin ribozyme #20.
 XX
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virolicide;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytosstatic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW substrate; hairpin ribozyme; HP ribozyme; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN US2002082225-A1.
 XX
 PD 27-JUN-2002.
 XX
 XX 23-MAR-1999; 99US-00274553.
 XX
 PR 23-MAR-1999; 99US-00274553.
 XX
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA (ROBE/) ROBERTS B.
 PA (PAVC/) PAVCO P A.
 PA (MACE/) MACEJACK D.
 XX
 PI Blatt L, Meswigen JA, Roberts B, Pavco PA, Macejack D;
 XX
 DR WPI; 2002-617759/66.
 XX
 PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
 PT replication and are useful to treat hepatitis C virus infections and
 PT cirrhosis, liver failure or hepatocellular carcinoma.
 XX
 PS Claim 2; Page 59; 80pp; English.
 XX
 CC The present invention relates to enzymatic nucleic acids which
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
 CC (HP) motif where the binding arms comprise sequences complementary to one
 CC of the substrate sequences defined in the specification. The HCV
 CC ribozymes are useful for modulating the expression and/or replication of
 CC HCV. They can be used to treat cirrhosis, liver failure and/or
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
 CC a condition associated with HCV infection in conjunction with one or more
 CC other drug therapies, particularly type I interferon, especially
 CC interferon alpha, beta or gamma or consensus interferon. The present
 CC sequence represents a substrate for a HCV hairpin (HP) ribozyme. Note:
 CC Some of the sequence data for this patent did not form part of the
 CC printed specification. The complete sequence data for this patent was
 CC obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/pslpsDIDEntry.html
 XX
 SQ Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
 Query Match 11.4%; Score 8.8; DB 1; Length 14;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAACAGACGGC 13

```

Db      14 AACACGACGACG 3
||||| ||| ||
RESULT 297
ID AEB76459/c
XX AEB76459 standard; RNA; 14 BP.
AC AEB76459;
XX
DT 22-SEP-2005 (first entry)
XX
DE Hepatitis C virus hairpin ribozyme substrate sequence.
XX
KW ribozyme; enzymatic nucleic acid molecule; hepatitis C virus infection;
KW antiviral; gene therapy; substrate; ss.
XX
OS Hepatitis C virus.
XX
PN US202013458-A1.
XX
PD 31-JAN-2002.
XX
PF 15-FEB-2000; 2000US-00504231.
XX
PR 23-MAR-1999; 99US-00274553.
XX
PA (BLATT/) BLATT L.
PA (MCSW/) MCSWIGGEN J A.
PA (ROBE/) ROBERTS E.
PA (PAVO/) PAVO P A.
PA (MACE/) MACEJACK D.
XX
PI Blatt L, Mcswiggen JA, Roberts E, Pavo PA, Macejack D;
XX
DR WPI; 2002-215899/27.
XX
DT New enzymatic nucleic acid molecule, which specifically cleaves minus
PT strand RNA derived from hepatitis C virus, useful for modulating the
PT expression and/or replication of hepatitis C virus.
XX
XX
XX Example 1; Page 43; 65pp; English.
XX
CC The invention relates to an enzymatic nucleic acid molecule which
CC specifically cleaves minus strand RNA derived from hepatitis C virus
CC (HCV). The binding arms of the molecule comprise ribozyme sequences. The
CC molecule is selected from inozyme, G-cleaver, DNazyme, Amberzyme, and
CC Zinzyme motifs. Also described: (1) a pharmaceutical composition
CC comprising the novel enzymatic nucleic acid; (2) a mammalian cell
CC including the novel enzymatic nucleic acid; (3) an expression vector
CC comprising a nucleic acid sequence encoding at least one enzymatic
CC nucleic acid molecule, in a manner, which allows expression of that
CC molecule; (4) a mammalian cell including an expression vector of (3); (5)
CC methods for treating cirrhosis, liver failure or hepatocellular carcinoma
CC by administering to a patient the novel enzymatic nucleic acid or the
CC vector of (3); (6) a method of treating a patient having a condition
CC associated with HCV infection, by contacting cells of the patient with
CC the nucleic acid molecule, and further employing one or more drug
CC therapies; (7) a method for inhibiting HCV replication in a mammalian
CC cell by administering the novel enzymatic nucleic acid; and (8) a method
CC of cleaving a separate RNA molecule by contacting the novel enzymatic
CC nucleic acid with the separate RNA molecule. The enzymatic nucleic acid
CC is useful for modulating the expression and/or replication of hepatitis C
CC virus (HCV), and for inhibiting the expression of HCV minus strand. The
CC nucleic acid may also be used to treat or prevent the occurrence of a
CC disease state in a patient. The present sequence represents an HCV
CC hairpin ribozyme target substrate sequence which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 14 BP; 0 A; 4 C; 3 G; 0 T; 7 U; 0 Other;
Query Match 11.4%; Score 8.8; DB 1; Length 14;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Indels 0; Gaps 0;

Db      2 AACACGACGACG 13
||||| ||| ||
Db      14 AACACGACGACG 3
||||| ||| ||
RESULT 298
ID AEB19896
XX AEB19896 standard; DNA; 15 BP.
AC AEB19896;
XX
DT 25-AUG-2005 (first entry)
XX
DE PCR primer #1.
XX
KW Microorganism detection; PCR; primer; intestine infection;
KW gastrointestinal-gen.; gastrointestinal disease; infection; ss.
XX
OS Vibrio fluvialis.
XX
PN CN1560273-A.
XX
PD 05-JAN-2005.
XX
PF 26-FEB-2004; 2004CN-00015461.
XX
PR 26-FEB-2004; 2004CN-00015461.
XX
PA (UYZH-) UNIV ZHONGSHAN.
XX
PI Deng X, He J, Wang Z;
XX
DR WPI; 2005-296834/31.
XX
DT Kit for diagnosing gene of pathogenic bacterial and river vibron of
PT aquatic animal and human and testing method thereof.
XX
XX
XX Claim 1; Page 2; 7pp; Chinese.
XX
CC The invention relates to a kit for detecting aquatic animal pathogens and
CC human pathogens, comprising a pair of PCR primers used to detect specific
CC DNA fragments of Vibrio fluvialis. The kit and method can be used in
CC bacteria tracking and detection of aquatic animal pathogens in the course
CC of breeding and also in the clinical detection of human intestinal acute
CC infections, as well as in environmental monitoring. This sequence
CC represents a PCR primer used in the scope of the invention.
XX
SQ Sequence 15 BP; 3 A; 6 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 11.4%; Score 8.8; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Indels 0; Gaps 0;

Db      34 TCCTCTGAGAGG 45
||||| ||| |||
Db      3 TCCTCCGAGG 14
||||| ||| |||
RESULT 299
ID ACF57644
XX ACF57644 standard; DNA; 10 BP.
AC ACF57644;
XX
DT 22-APR-2004 (first entry)
XX
DE Human ALDOB gene allele-specific primer SEQ ID NO: 95.
XX
KW Human; ALDOB; fructose-bisphosphate aldolase B; SNP;
KW single nucleotide polymorphism; primer; probe; ss.
XX

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OS Homo sapiens.
XX WO2003091454-A1.
XX
XX
XX PD 06-NOV-2003.
XX
XX PF 26-APR-2002; 2002WO-US013328.
XX
XX PR 26-APR-2002; 2002WO-US013328.
XX
XX PA (GENA-) GENAISSANCE PHARM INC.
XX
XX PI Chew A, Kazemi A, Koshiy B;
XX
XX DR WPI; 2003-877338/81.
XX
XX PS Claim 41; Page 15; Opp; English.
XX
XX CC The present invention provides the protein and coding sequences of human
CC fructose-bisphosphate aldolase B (ALDOB) and single nucleotide
CC polymorphisms (SNPs) which have been identified in each sequence. The
CC method of haplotyping the sequences is useful for haplotyping the
CC fructose-bisphosphate aldolase B (ALDOB) gene of an individual or for
CC validating the ALDOB protein as a candidate target for treating a medical
CC condition predicted to be associated with ALDOB activity. The present
CC sequence is an allele-specific primer/probe used to identify the
CC haplotype of the human ALDOB gene in the exemplification of the invention
XX
XX SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 10.9%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 35 CCTCTGAGAG 44
Db 1 CCTCTGAGAG 10

Search completed: April 19, 2006, 16:12:08
Job time : 0.001 secs
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